

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: June 8, 2003, 04:02:02 ; Search time 3845 Seconds
(without alignments)
10914.498 Million cell updates/sec

Title: US-09-938-703-3

Perfect score: 1442

Sequence: 1 GAAATCCCAACAGAGCCA.....AGTAGTAGATCCGAATTC 1442

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 2054640 seqs, 14551402878 residues

Total number of hits satisfying chosen parameters: 4109280

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

GenBank:

1: gb.ba.*

2: gb.htg.*

3: gb.in.*

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6: gb.pat.*

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40: en.htgo.mus.*

41: en.htgo.other.*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1442	100.0	1442	6	AX427283 Sequence
2	1417.2	98.3	7422	9	AF009962 Homo sapi
3	1382.8	95.9	1477	6	AX153803 Sequence
4	1382.8	95.9	1477	6	AX427281 Sequence
5	1375.2	95.4	6059	9	HSCCR5AB2
6	1375.2	95.4	143068	6	AX335952 Sequence
7	1375.2	95.4	143068	9	HSU95626
8	1375.2	95.4	185437	9	AC098613 Homo sapi
9	1344	93.2	1344	6	AR119948 Sequence
10	1302	90.3	1376	6	AR119946 Sequence
11	1302	90.3	1376	9	HSCCKRAG
12	1293.4	89.7	1414	6	AX297794 Sequence
13	1293.4	89.7	1414	6	AX297803 Sequence
14	1293.4	89.7	1414	6	AX297812 Sequence
15	1293.4	89.7	1414	6	AX297821 Sequence
16	1293.4	89.7	1414	6	AX297830 Sequence
17	1293.4	89.7	1414	6	AX297839 Sequence
18	1288.6	89.4	1414	6	BD006753
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20	1149	79.7	3383	6	AR161694
21	1149	79.7	3383	6	BD006760 Chemokine
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23	1117	77.5	1225	6	AX256200 Sequence
24	1117	77.5	1225	9	HSU57840
25	1115.4	77.4	1225	6	AX256202 Sequence
26	1027	71.2	1027	9	HSCMKBR5
27	1027	71.2	1027	9	HSU66285
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35	982.8	68.2	1060	9	AF011506 Homo sapi
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37	982.8	68.2	1060	9	AF011510 Homo sapi
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ALIGNMENTS

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LOCUS	Sequence 5 from Patent EP1199360.				
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ACCESSION	AX427283				
VERSION	AX427283.1	GI:21530636			
KEYWORDS	unidentified.				
SOURCE	unidentified				
ORGANISM	unclassified.				
REFERENCE	1				
AUTHORS	Samson, M., Parmentier, M., Vassart, G. and Libert, F.				
TITLE	Active and inactive cc-chemokine receptors and nucleic acid				
JOURNAL	molecules encoding said receptor				
	Patent: EP 1199360-A 5 24-APR-2002;				

Euroscreen S.A. (BE)
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RESULT 2

AF009962
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 DEFINITION AF009962
 ACCESSION AF009962
 VERSION AF009962.1 GI:3243092
 KEYWORDS
 SOURCE Homo sapiens.
 ORGANISM Homo sapiens

REFERENCE

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 Tse, L., Ehsenberg, P. K., Chang, G. and Michael, N. L.
 Genomic Organization and Functional Characterization of the Complete Transcription Unit for the Chemokine Receptor CCR-5, a Major Entry Co-Receptor for HIV-1

JOURNAL

Unpublished
 Tse, L., Ehsenberg, P. K., Chang, G. and Michael, N. L.
 Direct Submission
 Submitted (23-JUN-1997) Div. of Retrovirology, Walter Reed Army Institute of Research, 13 Taft Court, Suite 200, Rockville, MD 20850, USA

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RESULT 5
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LOCUS HSCCR5AB2 6059 bp DNA linear PRI 03-JAN-1998
DEFINITION Homo sapiens CC chemokine receptor 5 (CCR5) gene, complete cds.
ACCESSION AF031237
VERSION AF031237.1 GI:2739497
KEYWORDS
SEGMENT 2 of 2
SOURCE Homo sapiens
ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 5059)
AUTHORS Mammalia; Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
TITLE The human CC chemokine receptor 5 (CCR5) gene. Multiple transcripts with 5'-end heterogeneity, dual promoter usage, and evidence for polymorphisms within the regulatory regions and noncoding exons
J. Biol. Chem. 272 (49), 30662-30671 (1997)
JOURNAL 98049523
MEDLINE 9388201
PUBMED
REFERENCE 2 (bases 1 to 6059)
AUTHORS Mummidi,S., Ahuja,S.S., McDaniel,B.L. and Ahuja,S.K.

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RESULT 6
AX335952
LOCUS AX335952 143068 bp DNA linear PAT 09-JAN-2002
DEFINITION Sequence 6461 from Patent WO0194629.
ACCESSION AX335952
VERSION AX335952.1 GI:18126671
KEYWORDS human.
SOURCE Homo sapiens
ORGANISM Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
REFERENCE 1
AUTHORS Young,P.E., Augustus,M., Carter,K.C., Ebner,R., Endress,G.,
Horrigan,S., Soppet,D.R. and Weaver,Z.
TITLE Cancer gene determination and therapeutic screening using signature
gene sets
JOURNAL Patent: WO 0194629-A 6461 13-DEC-2001;
Avalon Pharmaceuticals (US)
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Best Local Similarity 97.4%; Pred. No. 0; Mismatches 3; Indels 35; Gaps 2;
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QY 181 AATATACATCTAGGACATTTATAAGATCACTTTTATTTATGCACAGGTTGGAACAAGA 240
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Db 62084 TGGGGCTGTGCTGGCTGTGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 62143
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QY 1347 -TTGGAGGCTCTTTTAAAGAGAGTACTGTTATAGAGGCTTAAGATTATCATCTCTT 1405
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 DEFINITION (ccr5) genes, complete cds, and lactoferrin (lactoferrin) gene,
 partial cds, complete sequence.
 ACCESSION U95626
 VERSION U95626.1 GI:2104517
 KEYWORDS HTG.
 SOURCE Homo sapiens.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 1 (bases 1 to 143068)
 McCombie, W.R., Wilson, R., Chen, E., Gibbs, R., Zuo, L., Johnson, D.,
 Nhan, M., Parnell, L., Dedhia, N., Ansari, A., Mardis, E., Schutz, K.,
 Gnoj, L., de la Bastide, M., Kaplan, N., Greco, T., Touchman, J.,
 Muzny, D., Chen, C.-N., Evans, C., Fitzgerald, M., See, L.H., Tang, M.,
 Porcel, B.M., Dragan, Y., Giacalone, J., Pae, A., Powell, E.,
 Solinsky, K.A., Desilva, U., Diaz-Perez, S., Zhou, X., Yu, Y.,
 Watanabe, M., Doggett, N., Garcia, D. and Sagripanti, J.-L.
 Human BAC clone 110P12
 Unpublished (1997)
 2 (bases 1 to 143068)
 McCombie, R.W., Wilson, R., Chen, E., Gibbs, R., Zuo, L., Johnson, D.,
 Nhan, M., Parnell, L., Dedhia, N., Ansari, A., Mardis, E., Schutz, K.,
 Gnoj, L., de la Bastide, M., Kaplan, N., Greco, T., Touchman, J.,
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 Porcel, B.M., Dragan, Y., Giacalone, J., Pae, A., Powell, E.,
 Solinsky, K.A., Desilva, U., Diaz-Perez, S., Zhou, X., Yu, Y.,
 Watanabe, M., Doggett, N., Garcia, D. and Sagripanti, J.-L.
 Direct Submission
 TITLE Submitted (27-MAR-1997) Advanced Genome Sequence Analysis Course,
 Cold Spring Harbor Laboratory, 1Bungtown Rd., Cold Spring Harbor,
 NY 11724, USA
 COMMENT Regions with single-strand coverage are as follows:

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 59166 - 59206 63708 - 63998 65200 - 65335
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DEFINITION Homo sapiens chromosome 3 clone RP11-24F11, complete sequence.
ACCESSION AC098613
VERSION AC098613.2 GI:22038607
KEYWORDS HTG.
SOURCE human.
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
AUTHORS Kaul, R.K., Olson, M.V., Zhou, Y., James, R.A., Rouse, G., Wu, Z., Saenphimmachak, C., Phelps, K.A., Buckley, D., Kibukawa, M., Raymond, C. and Haugen, E.D.
TITLE Direct Submission
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 185437)
AUTHORS Kaul, R.K., Olson, M.V., Raymond, C. and Haugen, E.D.
TITLE Direct Submission
JOURNAL Submitted (26-OCT-2001) Genome Center, University of Washington, Box 352145, Seattle, WA 98195, USA
REFERENCE 3 (bases 1 to 185437)
AUTHORS Kaul, R.K., Olson, M.V., Zhou, Y., James, R.A., Rouse, G., Wu, Z., Saenphimmachak, C., Phelps, K.A., Buckley, D., Kibukawa, M., Raymond, C. and Haugen, E.D.
TITLE Direct Submission
JOURNAL Submitted (01-AUG-2002) Genome Center, University of Washington, Box 352145, Seattle, WA 98195, USA
COMMENT On Aug 1, 2002 this sequence version replaced gi:16445164.

Center: University of Washington Genome Center
Center Code: UWGC
Web site: <http://www.genome.washington.edu>
Contact: uwgchaseu.washington.edu

Project Information
Center project name: chr-3
Center clone name: RP11-24F11 (bc0137)

Summary Statistics
Sequencing vector: plasmid; 100% of reads
Chemistry: Dye-terminator ET; 93% of reads
Chemistry: Dye-terminator Big Dye; 7% of reads
Assembly program: Phrap; version 0.990319
Consensus quality: 184860 bases at least Q40
Consensus quality: 185398 bases at least Q30
Consensus quality: 185435 bases at least Q20
Insert size: 185437; sum-of-contigs
Quality coverage: 7.6x in Q20 bases; sum-of-contigs

Overlapping Sequences:
5': BAC-110P12 U95626, 111014-bp overlap
3': RP11-509121 (UWGC:bc0454) AC104304, 61294-bp overlap

Sequence Quality Assessment:
This entry has been annotated with sequence quality estimates computed by the Phrap assembly program. All manually edited bases have been reduced to quality zero. Quality levels above 40 are expected to have less than 1 error in 10,000 bp.
Base-by-base quality values are not generally visible from the GenBank flat file format but are available as part of this entry's ASN.1 file.

This sequence was finished as follows unless otherwise noted:
all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., Phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest.

Sequence Validation:
This sequence has been validated by Multiple Complete Digest fingerprinting. Comparison of the experimentally derived digest fragments with sequence-predicted fragments is given below.
The electronically-digested sequence consists of both insert and

vector, in order to accurately represent the entire circular BAC. Small fragments below a variable cutoff (approximately 400-800 bp) are not resolved in the fingerprint and hence do not appear in the table. There are no significant remaining discrepancies between the experimental and predicted values. Uniquely ordered fragments are separated by dashed lines.

BgIII				EcoRI				HindIII			
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2067	2065	6	<800	6382	6501						
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5681	5720	1846	1824	512	<800						
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3716	3953	4052	3986	449	<800						
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875	897	1159	1130	6692	6501						
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910	897	54	<800	10449	10229						
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2169	2215	560	<800	953	1025						
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1705	1653	2287	2267	3124	3176						
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5763	5720	4905	4891	1054	1025						
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5844	5720	3049	3078	3985	3998						
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5061	5001	1377	1394	1100	1025						
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2625	2640	9903	9772	124	<800						
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725	<800	1022	1021	2671	2693						
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1173	1161	12606	12503	1948	1968						
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5747	5720	866	868	83	<800						
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9995	9684	9817	9772	7455	7474						
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999	999	3598	3601	1305	1267						
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4541	4503	452	<800	1047	1025						
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2950	2981	7549	7635	3299	3301						
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406	<800	2063	2075	5279	5237						
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416	<800	4104	3986	2509	2576						
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287	<800	2758	2771	7758	7830						
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9428	9684	1307	1304	11020	10820						
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3809	3953	13306	13328	1978	1968						
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1275	1234	2423	2450	8741	8681						
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3351	3381	2243	2267	4795	4815						

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DB	421 TGAAGAGCATGACTGACTCACTACCTGCTCAACTGCTGCAACTGCGCATCTGACCTGTTTCTTC 480		
QY	481 TTACTGTCCCTCTTGGCTCACTATGCTGCGCCAGTGGGACTTTGGAATACATGT 540		
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DEFINITION Sequence 1 from Patent EP1145721.
ACCESSION AX297821
VERSION AX297821.1 GI:17065857
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SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
Li, Y. and Ruben, S. M.
Human g-protein chemokine receptor hGnrl10 (ccr5 receptor).
Pharmaceutical composition
Patent: EP 1145721-A 1 17-OCT-2001;
HUMAN GENOME SCIENCES, INC. (US)
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ORIGIN

Query Match 89.7%; Score 1293.4; DB 6; Length 1414;
Best Local Similarity 96.6%; Pred. No. 0;
Matches 1345; Conservative 0; Mismatches 16; Indels 32; Gaps 1;

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Job time : 3850 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: June 8, 2003, 00:19:22 ; Search time 357 Seconds
(without alignments)
9096.307 Million cell updates/sec

Title: US-09-938-703-3

Perfect score: 1442

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Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 2185239 seqs, 112599159 residues

Total number of hits satisfying chosen parameters: 4370478

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query	Score	Match	Length	ID	Description
1	1442	100.0	1442	18	AAT90118	cDNA for inactive
2	1382.8	95.9	1477	18	AAT90117	cDNA for human CCR
3	1382.8	95.9	1477	22	AAF87059	Human CCR5 cDNA se
4	1375.2	95.4	9141	24	ABA97318	Human chemokine (C
5	1375.2	95.4	143068	21	AAF21105	Human low adenosin
6	1375.2	95.4	143068	21	AAF21272	Human low adenosin
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8	1375.2	95.4	143068	21	AAA35150	Human adenosine re
9	1375.2	95.4	143068	21	ABJ68124	Ovary cancer relat
					AAA35151	Human adenosine re

10	1375.2	95.4	152740	21	AAF21273	Human low adenosin
11	1373.6	95.3	143068	21	AAA34983	Human adenosine re
12	1344	93.2	1344	20	AAV84159	HIV-1 co-receptor
13	1302	90.3	1376	22	AAH26903	Human HIV-1 co-rec
14	1299	90.1	1376	22	AAV84126	HIV-1 co-receptor
15	1293.4	89.7	1414	20	AAF26390	Human HDGNR10 cDNA
16	1288.6	89.4	1414	18	AAT44042	Human G-protein ch
17	1288.6	89.4	1414	21	AAZ91481	Human G-protein ch
18	1288.6	89.4	1414	22	AAI3181	Human G-protein ch
19	1288.6	89.4	1414	22	AAI3181	Human G-protein ch
20	1288.6	89.4	1414	24	AAI3181	Human G-protein ch
21	1160	80.4	1557	18	AAI3181	DNA encoding human
22	1149	79.7	3383	18	AAI3181	Human chemokine re
23	1149	79.7	3383	21	AAI3181	Human chemokine re
24	1149	79.7	3383	21	AAI3181	Human low adenosin
25	1149	79.7	3383	21	AAI3181	Human adenosine re
26	1117	77.5	1225	19	AAI3181	Human chemokine re
27	1117	77.5	1225	19	AAI3181	DNA encoding human
28	1115.4	77.4	1225	24	AAI3181	Human CC chemokine
29	1100	76.3	1255	19	AAI3181	Human CCR5 Gln 55
30	985	68.3	1059	19	AAI3181	DNA encoding human
31	985	68.3	1059	24	AAI3181	Human CC-CR5 codi
32	983.4	68.2	1071	20	AAI3181	Human chemokine (C
33	982.8	68.2	5674	20	AAI3181	HIV-1 co-receptor
34	981.8	68.1	1059	23	AAI3181	Human chemokine re
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36	980.4	68.0	1056	22	AAI3181	Human G-protein ch
37	980.4	68.0	1056	24	AAI3181	Human G-protein ch
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39	948.2	65.8	1059	18	AAI3181	Nucleotide sequenc
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41	727.4	50.4	2440	19	AAI3181	cDNA for inactive
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43	681.6	47.3	1083	22	AAI3181	Human monocyte che
44	680	47.2	1083	22	AAI3181	Human CCR2-641 pol
45	676.8	46.9	1083	18	AAI3181	Human wild-type CC
						Human monocyte che

ALIGNMENTS

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XX DT 14-APR-1998 (first entry)
XX DE cDNA for inactive human CCR5.
XX KW Inactive; human Cys-Cys chemokine receptor 5; CCR5;
KW human immunodeficiency virus; type 1; type 2; HIV-1; HIV-2;
KW predisposition; resistance; diagnosis; treatment; prevention;
KW inflammatory disease; rheumatoid arthritis; glomerulonephritis;
KW asthma; idiopathic pulmonary fibrosis; psoriasis; viral infection;
KW cancer; atherosclerosis; autoimmune disorder; ss.
XX OS Homo sapiens.

XX Key Location/Qualifiers
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XX PN W09732019-A2.
XX PD 04-SEP-1997.
XX PF 28-FEB-1997; 97WO-BE00023.
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KW cancer; atherosclerosis; autoimmune disorder; ss.
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 XX Libert F, Parmentier M, Samson M, Vassart G;
 XX WPI: 1997-479829/44.
 XX P-PSDB; RAT90117.
 XX
 XX Active and inactive forms of human CC chemokine receptor CCR-5 -
 XX useful to diagnose, prevent and/or treat inflammatory disorders,
 XX autoimmune disease and viral infection
 XX
 XX Claim 18; Fig 1b-c; 94pp; English.
 XX
 XX The present sequence encodes human CC (Cys-Cys) chemokine receptor
 XX 5 (CCR5), which is stimulated by MIP-1 alpha, MIP-1 beta or RANTES
 XX chemokines, but not by monocyte chemoattractant protein 1 (MCP-1),
 XX MCP-2, MCP-3, interleukin-8 (IL-8) or growth related gene product
 XX alpha (GRO alpha) chemokines. Active CCR-5 is also a receptor of
 XX human immunodeficiency virus type 1 or type 2 (HIV-1 or HIV-2).
 XX CCR5 or its cDNA can be used to diagnose, treat and/or prevent
 XX inflammatory diseases, e.g. rheumatoid arthritis,
 XX glomerulonephritis, asthma, idiopathic pulmonary fibrosis and
 XX psoriasis, viral infections, especially HIV-1 or HIV-2 infection,
 XX cancer, atherosclerosis and autoimmune disorders.
 XX
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 DB GATCCACTGGGAGGAGGAAATATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1320
 QY ACCAGTCAAGTGTGCAATGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1348
 DB ACCAGTCAAGTGTGCAATGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1380
 QY GG---GAGGCTTTTAAAGAGAGTACTGTTATAGAGGCTTAAGATTCATCCATTT 1405
 DB TGGNAGGCTTTTAAAGAGAGTACTGTTATAGAGGCTTAAGATTCATCCATTT 1440
 QY ATTTGGCATCTGTTTAAAGTATAGTCCGAATTC 1442
 DB ATTTGGCATCTGTTTAAAGTATAGTCCGAATTC 1442


```
QY 1109 GGGAGAAGTTCAGAACTACCTCTTAGCTCTTCCAAAAGCAGCAATGCCAAACGGTCTT 1168
D 1141 GGGAGAAGTTCAGAACTACCTCTTAGCTCTTCCAAAAGCAGCAATGCCAAACGGTCTT 1200
QY 1169 GCAAAATGCTGTTCTATTTCCAGCAAGAGGCTCCCGAGCGAGCAAGCTCAGTTACACCC 1228
D 1201 GCAAAATGCTGTTCTATTTCCAGCAAGAGGCTCCCGAGCGAGCAAGCTCAGTTACACCC 1260
QY 1229 GATCCACTGGGAGCAGGAATAATCTGTGGGCTTGTGACACGAGCTCAAGTGGGCTGGTG 1288
D 1261 GATCCACTGGGAGCAGGAATAATCTGTGGGCTTGTGACACGAGCTCAAGTGGGCTGGTG 1320
QY 1289 ACCCACTCAGAGTGTGCAATGGCTTAGTTTTCATACACAGCTGGGCTGGGCTGGT 1348
D 1321 ACCCACTCAGAGTGTGCAATGGCTTAGTTTTCATACACAGCTGGGCTGGGCTGGT 1380
QY 1349 GG---GAGGCTCTTTTAAAGGAAGTACTGTTATAGAGGGTCTAAGATTCATCCATTT 1405
D 1381 TGGNAGGCTCTTTTAAAGGAAGTACTGTTATAGAGGGTCTAAGATTCATCCATTT 1440
QY 1406 ATTTGGCATCTGTTTAAAGTAGATATAGATCCGAATTC 1442
D 1441 ATTTGGCATCTGTTTAAAGTAGATATAGATCCGAATTC 1477

RESULT 4
ID ABA97318 standard; DNA; 9141 BP.
AC ABA97318;
XX
DT 18-JUN-2002 (first entry)
XX
DE Human chemokine (C-C motif) receptor 5 gene.
XX
KW Human chemokine C-C motif receptor 5; CCR5; haplotype pair; isogene;
KW single nucleotide polymorphism; SNP; human immunodeficiency virus 1;
KW HIV-1 infection; acquired immunodeficiency syndrome; AIDS; antiviral;
KW genotype; polymorphic variant; transgenic; drug screening; gene therapy;
KW gene; chromosome 3p21; ds.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT variation replace (1629,A)
FT /tag= a
FT /standard_name= "Single nucleotide polymorphism"
FT variation replace (1953,C)
FT /tag= b
FT /standard_name= "Single nucleotide polymorphism"
FT variation replace (1956,T)
FT /tag= c
FT /standard_name= "Single nucleotide polymorphism"
FT variation replace (2002,A)
FT /tag= d
FT /standard_name= "Single nucleotide polymorphism"
FT variation replace (2253,T)
FT /tag= e
FT /standard_name= "Single nucleotide polymorphism"
FT variation replace (2402,C)
FT /tag= f
FT /standard_name= "Single nucleotide polymorphism"
FT variation replace (3920,T)
FT /tag= g
FT /standard_name= "Single nucleotide polymorphism"
FT CDS 4083..5141
FT /tag= h
FT /product= "CCR5"
FT /note= "Human chemokine (C-C motif) receptor 5"
FT variation replace (4246,A)
FT /tag= i
FT /standard_name= "Single nucleotide polymorphism"
FT variation replace (4307,C)
```

```
FT /tag= j
FT /standard_name= "Single nucleotide polymorphism"
FT variation replace (4403,T)
FT /tag= k
FT /standard_name= "Single nucleotide polymorphism"
FT variation replace (4628,G)
FT /tag= l
FT /standard_name= "Single nucleotide polymorphism"
FT variation replace (4750,A)
FT /tag= m
FT /standard_name= "Single nucleotide polymorphism"
XX
PN W0200177125-A2.
XX
PD 18-OCT-2001.
XX
PF 04-APR-2001; 2001WO-US10708.
XX
PR 05-APR-2000; 2000US-194361P.
XX
PA (GENA-) GENAISSANCE PHARM INC.
XX
PI Choi JY, Klieem SE, Koshy B;
XX
DR WPI; 2002-041282/05.
DR P-PSDB; ABH08343.
XX
PT New haplotypes of the human chemokine (C-C motif) receptor 5 gene,
PT useful to diagnose and treat diseases associated with its abnormal
PT expression or function, including human immunodeficiency virus-1
PT infection -
XX
PS Claim 21; Fig 1; 61pp; English.
XX
CC The present sequence represents the human chemokine (C-C motif) receptor
CC 5 (CCR5) gene of the invention which encodes the polypeptide given in
CC AB080343. The specification describes haplotyping the CCR5 gene of an
CC individual by determining if the individual has one of the CCR5
CC haplotypes or haplotype pairs fully defined in the specification. The
CC specification also describes an isolated polynucleotide comprising a
CC nucleotide sequence which is a polymorphic variant of the reference CCR5
CC gene sequence and comprises an isogene defined by a haplotype described
CC in the specification and its encoded polypeptide. The methods of the
CC invention are useful to diagnose and develop treatment for diseases
CC associated with abnormal expression or function of the gene. The CCR5
CC isogenes and the screened compounds are useful for treating human
CC immunodeficiency virus (HIV)-1 infection and the progression to acquired
CC immunodeficiency syndrome (AIDS). The invention has antiviral
CC applications. The specification describes genotyping the CCR5 gene of an
CC individual; predicting a haplotype pair for the CCR5 gene of an
CC individual; identifying an association between a trait and a haplotype or
CC haplotype pair of the CCR5 gene. The specification describes a
CC composition comprising a genotyping oligonucleotide for detecting a CCR5
CC polymorphism; a recombinant non-human organism transformed with CCR5
CC polynucleotide expressing a CCR5 protein encoded by the variant sequence;
CC an isolated antibody specific for the CCR5 polypeptide and a method for
CC screening drugs targeting the CCR5 polypeptide.
XX
SQ Sequence 9141 BP; 2596 A; 1853 C; 2065 G; 2627 T; 0 other;
```

```
Query Match 95.4%; Score 1375.2; DB 24; Length 9141;
Best Local Similarity 97.4%; Pred. No. 0;
Matches 1432; Conservative 0; Mismatches 3; Indels 35; Gaps 2;

QY 1 GAATTCCTCCCAACAGAGCCAGCTCTCCATCTAGTGAGGGAAGCTAGCAGCAACCT 60
D 3844 GAATTCCTCCCAACAGAGCCAGCTCTCCATCTAGTGAGGGAAGCTAGCAGCAACCT 3903
QY 61 TCCCTTCACATACAAACTTCATTCCTTGGCCAAAAGAGAGTTAATTCATGTAGCATC 120
D 3904 TCCCTTCACATACAAACTTCATTCCTTGGCCAAAAGAGAGTTAATTCATGTAGCATC 3963
QY 121 TATGTAGGCAATTAATAAACCTATTGATGATATAAACAGTTTGGCATTCATGGAGGCAACT 180
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Db 3964 TATGTAGGCAATTAATAAACCTTATGTATATAAACAGTTTGCAATTCATGGAGGCAACT 4023
QY 181 AAATACATCTAGGACTTTAAAGATCACTTTTATTTATGACAGAGGTTGGAACAAGA 240
Db 4024 AAATACATCTAGGACTTTAAAGATCACTTTTATTTATGACAGAGGTTGGAACAAGA 4083
QY 241 TGGATTATCAAGTGTCAAGTCCATCTATGACATCAATATATACATCGGAGCCCTGCC 300
Db 4084 TGGATTATCAAGTGTCAAGTCCATCTATGACATCAATATATATACATCGGAGCCCTGCC 4143
QY 301 AAAAATCAATGTGAAGCAAAATCGAGCCGCCCTCTGCGCTCCGCTCTACTACTGTGT 360
Db 4144 AAAAATCAATGTGAAGCAAAATCGAGCCGCCCTCTGCGCTCCGCTCTACTACTGTGT 4203
QY 361 TCATCTTTGGTTTTTGGGCAACATGCTGTCATCCATCCCTGATTAACACTGCAAAAGGC 420
Db 4204 TCATCTTTGGTTTTTGGGCAACATGCTGTCATCCCTGATTAACACTGCAAAAGGC 4263
QY 421 TGAAGACATGACTGACATCTACCTGCTCAACCTGGCCATCTCTGACCTGTTTTTCCCTTC 480
Db 4264 TGAAGACATGACTGACATCTACCTGCTCAACCTGGCCATCTCTGACCTGTTTTTCCCTTC 4323
QY 481 TTACTGTCCTCTCTGGCTCAGTATGCTGCGGCCAGTGGGACITTTGGAATCAATGT 540
Db 4324 TTACTGTCCTCTCTGGCTCAGTATGCTGCGGCCAGTGGGACITTTGGAATCAATGT 4383
QY 541 GTCAACTCTTGACAGGCTCTATTTATAGGCTTCTCTGGAATCTTCTTCATCATCC 600
Db 4384 GTCAACTCTTGACAGGCTCTATTTATAGGCTTCTCTGGAATCTTCTTCATCATCC 4443
QY 601 TCCGACATTCGATGAGTACCTGGCTGCTGCTCCAGTCTGTTGTTGTTAAAGCCAGGA 660
Db 4444 TCCGACATTCGATGAGTACCTGGCTGCTGCTCCAGTCTGTTGTTGTTAAAGCCAGGA 4503
QY 661 CGGTACCTTTGGGTGGTGACAGTGTGATCACTTGGGTGGTGGTGGTGGTGGTGGT 720
Db 4504 CGGTACCTTTGGGTGGTGACAGTGTGATCACTTGGGTGGTGGTGGTGGTGGTGGT 4563
QY 721 TCCAGGAATCATCTTTACAGATCTCAAAAGAGTGTCTTCAATACACTGACAGTCTC 780
Db 4564 TCCAGGAATCATCTTTACAGATCTCAAAAGAGTGTCTTCAATACACTGACAGTCTC 4623
QY 781 ATTTTCCAT-----ACATTAAGATAGTCACT 808
Db 4624 ATTTTCCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 4683
QY 809 TGGGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 868
Db 4684 TGGGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 4743
QY 869 TGCTTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 928
Db 4744 TGCTTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 4803
QY 929 TGATTTGTTATTTCTCTCTGGGCTCCCTACACATGTCCTCTCTCTCTCTCTCTCTCTCT 988
Db 4804 TGATTTGTTATTTCTCTCTGGGCTCCCTACACATGTCCTCTCTCTCTCTCTCTCTCTCT 4863
QY 989 AGGAATCTTTGGCTGGAATTAATGACAGTGTCTACAGGTTGGACCAAGCTATGACAG 1048
Db 4864 AGGAATCTTTGGCTGGAATTAATGACAGTGTCTACAGGTTGGACCAAGCTATGACAG 4923
QY 1049 TGACAGAGATCTTTGGGATGACGACTGCTGATCAACCCATCATCTATGCTTTGTCG 1108
Db 4924 TGACAGAGATCTTTGGGATGACGACTGCTGATCAACCCATCATCTATGCTTTGTCG 4983
QY 1109 GGGAGAGTTTCAAGAACTACCTCTTAGTCTTTTCCAAAAGACATTTGCCAAAGCTTCT 1168
Db 4984 GGGAGAGTTTCAAGAACTACCTCTTAGTCTTTTCCAAAAGACATTTGCCAAAGCTTCT 5043
QY 1169 GCAATGCTGTTCTATTTTCCAGCAAGAGGCTCCGAGGAGCAAGCTCAGTTTACACCC 1228

Db 5044 GCAAAATGCTGTTCTATTTTCCAGCAAGAGGCTCCCGAGCGAGCAAGCTCAGTTTACACCC 5103
QY 1229 GATCCACTGGGGAGCAGGAATATCTGTGGCTGTGTGACACGAGCTCAAGTGGGCTGGT 1288
Db 5104 GATCCACTGGGGAGCAGGAATATCTGTGGCTGTGTGACACGAGCTCAAGTGGGCTGGT 5163
QY 1289 ACCAGTCCAGAGTGTGACATGCTTACTGTTTATACACAGCCCTGGGCTGGGCTGGT 1346
Db 5164 ACCAGTCCAGAGTGTGACATGCTTACTGTTTATACACAGCCCTGGGCTGGGCTGGT 5223
QY 1347 -TTGGAGGCTCTTTTAAAGGAAGTACTGTTATAGAGGCTTAAAGTTCATCATCATTT 1405
Db 5224 TGGGAGAGGCTCTTTTAAAGGAAGTACTGTTATAGAGGCTTAAAGTTCATCATCATTT 5283
QY 1406 ATTTGGCATCTGTTTAAAGTAGATTAGATC 1435
Db 5284 ATTTGGCATCTGTTTAAAGTAGATTAGATC 5313
RESULT 5
AAF21105
ID AAF21105 standard; DNA; 143068 BP.
XX AC AAF21105;
XX DT 14-MAR-2001 (first entry)
XX DE Human low adenosine antisense oligonucleotide related sequence #2672.
XX KW Low adenosine antisense oligonucleotide; phosphorothioate; allergy;
human; airway disorder; bronchoconstriction; lung inflammation;
surfactant depletion; respiratory; bronchodilator; antiinflammatory;
immunosuppressive; antiallergic; analgesic; hypotensive; cytostatic;
respiratory obstruction; pulmonary obstruction; impeded respiration;
surfactant hypoproduction; pulmonary vasoconstriction; asthma; RDS;
respiratory distress syndrome; pain; cystic fibrosis; allergic rhinitis;
pulmonary hypertension; emphysema; pulmonary transplantation rejection;
chronic obstructive pulmonary disease; pulmonary infection; bronchitis;
cancer; ss.
XX OS Homo sapiens.
XX PN W0200062735-A2.
XX PD 26-OCT-2000.
XX PF 24-MAR-2000; 2000WO-US08020.
XX PR 06-APR-1999; 99US-0127958.
XX PA (UYEC-) UNIV EAST CAROLINA.
XX PA (NYCE/) NYCE J W.
XX PI Nyce JW;
XX DR WPI; 2000-679539/66.
XX PT Low adenosine (A) content antisense oligonucleotides which do not
trigger adenosine receptors during metabolism, useful e.g. for treating
cancers and respiratory obstructions -
XX PS Disclosure; Page 924-957; 1592pp; English.
XX CC The present invention describes low adenosine (A) content antisense
oligonucleotides and compositions (I) comprising them. In the antisense
oligonucleotides the A is replaced by a 'Universal' or alternative base.
(I) can have respiratory, bronchodilator, antiinflammatory, analgesic,
immunosuppressive, antiallergic, hypotensive and cytostatic activities.
The antisense oligonucleotides and (I) can be used to down-regulate the
expression and or activity of target polypeptides associated with
lung/respiratory disorders and malignancies, such as stimulating and
activating peptide factors and transmitters, transcription factors,
immunoglobulins and antibodies, antibody receptors, cytokines and

QY	721	TCCAGGAATCATCTTTACCATGATCTCAAAAGAAGGTCTTCATTACACCTGCAGCTCTC	780
Db	61964	TCCAGGAATCATCTTTACCATGATCTCAAAAGAAGGTCTTCATTACACCTGCAGCTCTC	62023
QY	781	ATTTTCCAT-----ACATTTAAGATAGTCACT	808
Db	62024	ATTTTCCATACAGTCAGTATCATTTCTGAGAAATTTCCAGACATTAAGATAGTCACT	62030
QY	809	TGGGCTGGTCCTGGCGCTGCTTCTCATGGTCATCTGCTACTCGGGATCCTCAAAAATC	868
Db	62084	TGGGCTGGTCCTGGCGCTGCTTCTCATGGTCATCTGCTACTCGGGATCCTCAAAAATC	62143
QY	869	TGCTTCGGTGTCAAAATGAGAAAGAGGCGACAGGGCTGTGAGGCTTATCTTCACATCA	928
Db	62144	TGCTTCGGTGTCAAAATGAGAAAGAGGCGACAGGGCTGTGAGGCTTATCTTCACATCA	62203
QY	929	TGATTTGTTTATTTTCTCTTCTGGGCTCCCTCAACATTTGCTCTTCTCTCGACACCTTCC	988

DB 62204 TGATTGTTTATTTCTCTTCTGGGCTCCCTACAACATTGTCTCTCTGAAACACCTTCC 62263

QY 989 AGGAATCTTTGGCCTGAATTAATTCAGTAGCTCTAACAGGTTGGACCAAGTATCGAG 1048
=====

D6 62264 AGGAATCTTTGGCCTGAATTAATTCAGTAGCTCTAACAGGTTGGACCAAGTATCGAG 62323

QY	1049	TGACAGAGACTCTGGGATGACGCACTGCTGCATCAACCCCATCATCATGCGCTTTGGTGG	1108
Db	62324	TGACAGAGACTCTGGGATGACGCACTGCTGCATCAACCCCATCATCATGCGCTTTGGTGG	62383
QY	1109	GGGAGAGTTTCAGNACTACCTCTTAGTCTTCTTCCAAAGACAATGGCCAAACGCTTCT	1168
Db	62384	GGGAGAGTTTCAGNACTACCTCTTAGTCTTCTTCCAAAGACAATGGCCAAACGCTTCT	62443
QY	1169	GCAATGCTGTTCTATTTTCCAGCAAGAGGCTCCGAGGAGCAAGCTCAGTTTACACC	1228
Db	62444	GCAATGCTGTTCTATTTTCCAGCAAGAGGCTCCGAGGAGCAAGCTCAGTTTACACC	62503
QY	1229	GATCCACTGGGGAGCAGGAATATCTGTGGGCTTGTGCACACGGACTCAAGTGGCGTGGTG	1288
Db	62504	GATCCACTGGGGAGCAGGAATATCTGTGGGCTTGTGCACACGGACTCAAGTGGCGTGGTG	62563
QY	1289	ACCCAGTCAGAGTTGTGCACATGGCTTAGTTTTCATACACAGCTGGGCTGGGGGTGG--	1346
Db	62564	ACCCAGTCAGAGTTGTGCACATGGCTTAGTTTTCATACACAGCTGGGCTGGGGGTGGGG	62623
QY	1347	-TTGGGAGGCTTTTTTAAAAGGAAGTACTGTATATAGAGGGCTCTAAGATTCATCATTT	1405
Db	62624	TGGGAGAGGCTTTTTTAAAAGGAAGTACTGTATATAGAGGGCTCTAAGATTCATCATTT	62683
QY	1406	ATTGGCATCTGTTTAAAGTAGATTAGATC 1435	
Db	62684	ATTGGCATCTGTTTAAAGTAGATTAGATC 62713	
RESULT 6			
AAAF21272			
XX	XX	AAAF21272 standard; DNA; 143068 BP.	
XX	XX	AAAF21272;	
XX	XX	14-MAR-2001 (first entry)	
XX	XX	Human low adenosine antisense oligonucleotide related sequence #2839.	
XX	XX	Low adenosine antisense oligonucleotide; phosphorothioate; allergy;	
KW	KW	human; airway disorder; bronchoconstriction; lung inflammation;	
KW	KW	surfactant depletion; respiratory; bronchodilator; antiinflammatory;	
KW	KW	immunosuppressive; antisthmatic; analgesic; hypotensive; cytostatic;	
KW	KW	respiratory obstruction; pulmonary obstruction; impeded respiration;	
KW	KW	surfactant hypoproduction; pulmonary vasoconstriction; asthma; RDS;	
KW	KW	respiratory distress syndrome; pain; cystic fibrosis; allergic rhinitis;	
KW	KW	pulmonary hypertension; emphysema; pulmonary transplantation rejection;	
KW	KW	chronic obstructive pulmonary disease; pulmonary infection; bronchitis;	

RESULT 6

AAF21272

ID AAF21272 standard; DNA; 143068 BP.

XX AC AAF21272:

XX

DT 14-MAR-2001 (first entry)

Human low adenosine antisense oligonucleotide related sequence #2020

XX
sequence #2099.

KW Low adenosine antisense oligonucleotide; phosphorothioate; allergy;

KW human; airway disorder; bronchoconstriction; lung inflammation;
KW surfactant depletion; respiratory; bronchodilation; anti-inflammation;

[illegible]

KW respiratory obstruction; pulmonary obstruction; impeded respiration;

KW surfactant hypoproduction; pulmonary vasoconstriction; asthma; RDS;
respiratory distress syndrome; surfactant deficiency

KW respiratory distress syndrome; pain; cystic fibrosis; allergic rhinitis;
KW pulmonary hypertension; emphysema: pulmonary transplantation rejection:
KW

KW chronic obstructive pulmonary disease; pulmonary infection; bronchitis; chronic obstructive pulmonary disease; pulmonary infection; bronchitis;

Db 62504 GATCCACTGGGAGCAGCAAAATATCTGGGCTTGTGACAGGACTCAAGTGGGCTGGTG 62563
QY 1289 ACCAGTCAGAGTTGTGCATGGCTTAGTTTTCATACACAGCCCTGGGCTGGGCTGGG 1346
Db 62564 ACCAGTCAGAGTTGTGCATGGCTTAGTTTTCATACACAGCCCTGGGCTGGGCTGGG 62623
QY 1347 -TTGGGAGGCTCTTTTAAAGGAAGTACTAGTTTATAGAGGCTTAAGATTCATCATTT 1405
Db 62624 TGGGAGAGGCTCTTTTAAAGGAAGTACTAGTTTATAGAGGCTTAAGATTCATCATTT 62683
QY 1406 ATTGGCATCTCTTTAAAGTACATAGATC 1435
Db 62684 ATTGGCATCTCTTTAAAGTACATAGATC 62713
RESULT 7
AAA35150
ID AAA35150 standard; DNA; 143068 BP.
XX AAA35150;
AC
DT 28-JUL-2000 (first entry)
XX
DE Human adenosine receptor related polynucleotide 2nd SEQ ID NO:24.
XX
KW Human; adenosine receptor; low adenosine antisense oligonucleotide;
KW phosphorothioate; impaired respiration; inflammation; allergy;
KW allergic disease; bronchoconstriction; inhibitor; antiinflammatory;
KW antiallergic; antiasthmatic; cytosstatic; analgesic; impaired airway;
KW lung disease; ischaemic condition; pulmonary vasoconstriction; asthma;
KW respiratory distress syndrome; pain; cystic fibrosis; emphysema;
KW pulmonary hypertension; chronic obstructive pulmonary disease; COPD;
KW cancer; leukaemia; lymphoma; carcinoma; metastasis; ss.
XX
OS Homo sapiens.
XX
PN WO200009525-A2.
XX
PD 24-FEB-2000.
XX
PF 03-AUG-1999; 99WO-US17712.
XX
PR 03-AUG-1998; 98US-0095212.
XX
PA (UYEC-) UNIV EAST CAROLINA.
XX
PI Nyce JW;
XX
WP1; 2000-205971/18.
XX
DR New antisense oligonucleotides useful for treating e.g. pulmonary
PT vasoconstriction, inflammation, allergies, asthma, hypertension,
PT bronchitis, emphysema, respiratory distress syndrome, ischemia or
PT cancers -
XX
PS Disclosure; Page 1106-1138; 1343pp; English.
XX
CC The present invention describes a new composition comprising an
CC antisense oligonucleotide (ON) with low adenosine (up to 15%), which
CC targets nucleic acids involved in bronchoconstriction, allergies, and/or
CC inflammation. The ON can have antiinflammatory, antiallergic,
CC antiasthmatic, cytosstatic and analgesic activities. The compositions are
CC useful for the treatment of diseases associated with inflammation,
CC impaired airways, including lung disease and diseases whose secondary
CC effects afflict the lungs of a subject. They can be used for treating
CC e.g. ischaemic conditions, pulmonary vasoconstriction, allergies,
CC asthma, impeded respiration, respiratory distress syndrome, pain, cystic
CC fibrosis, pulmonary hypertension, emphysema, chronic obstructive
CC pulmonary disease (COPD), and cancers such as leukaemias, lymphomas,
CC carcinomas, and cancers which may metastasise to the lungs, including
CC breast and prostate cancer. The reduction of the adenosine content of
CC the ONs reduces side effects. The A-containing ONs break down with the

CC release of deoxyadenosine which activates adenosine receptors causing
CC bronchoconstriction and inflammation. AAA32313 to AAA35312 represent the
CC nucleotide sequences given in the sequence listing from the present
CC invention, which correspond to SEQ ID NO:1 to 2815, and then the last
CC 185 sequences are also called SEQ ID NO:1 to 185, but the sequences
CC differ from the previously named sequences. SEQ ID NO:11 to 1690
CC (AAA32323 to AAA33992) are specifically claimed ONs from the present
CC invention. N.B. Sequences given in the disclosure of the present
CC invention do not match up with their corresponding SEQ ID NO: sequences
CC given in the sequence listing.

XX
SQ Sequence 143068 BP; 41194 A; 30126 C; 32402 G; 39346 T; 0 other;

Query Match 95.4%; Score 1375.2; DB 21; Length 143068;
Best Local Similarity 97.4%; Pred. No. 0;
Matches 1432; Conservative 0; Mismatches 3; Indels 35; Gaps 2;

QY 1 GAATTCCTCCCAACAGAGCCAGCTTCCTATCTAGTGGACAGGGAAGCTAGCAGCAACCT 60
Db 61244 GAATTCCTCCCAACAGAGCCAGCTTCCTATCTAGTGGACAGGGAAGCTAGCAGCAACCT 61303
QY 61 TCCCTTCCTACATAAAACTTCAATTCCTTGGCCAAAAGAGGTTAATTCATGTAGCATC 120
Db 61304 TCCCTTCCTACATAAAACTTCAATTCCTTGGCCAAAAGAGGTTAATTCATGTAGCATC 61363
QY 121 TATGTAGGCAATTAATAACCTATTGATGTATATAAACAGTTTGCATTCATGGAGGCAACT 180
Db 61364 TATGTAGGCAATTAATAACCTATTGATGTATATAAACAGTTTGCATTCATGGAGGCAACT 61423
QY 181 AAATACATCTTAGGACTTTATAAAGATCACATTTTATTTATGCACAGGTTGGACAGA 240
Db 61424 AAATACATCTTAGGACTTTATAAAGATCACATTTTATTTATGCACAGGTTGGACAGA 61483
QY 241 TGGATTATCAAGTGTCAAGTCCAAATCTATGACATCAATTAATATACATCGAGCCCTGCC 300
Db 61484 TGGATTATCAAGTGTCAAGTCCAAATCTATGACATCAATTAATATACATCGAGCCCTGCC 61543
QY 301 AAAAATCAATGTGAAGCAAAATCCAGCCGCCCTCTCCCTCCGCTCTACTCATCTGGTGT 360
Db 61544 AAAAATCAATGTGAAGCAAAATCCAGCCGCCCTCTCCCTCCGCTCTACTCATCTGGTGT 61603
QY 361 TCATCTTTGGTTTGGGCAACATGTGTCTCATCTCATCTCCCTGATAAACTGCAAAAGGC 420
Db 61604 TCATCTTTGGTTTGGGCAACATGTGTCTCATCTCATCTCCCTGATAAACTGCAAAAGGC 61663
QY 421 TGAAGAGCATGACTGACATCTACCTGCTCAACCTGECCTCTCTGACCTGTTTTCCTTC 480
Db 61664 TGAAGAGCATGACTGACATCTACCTGCTCAACCTGECCTCTCTGACCTGTTTTCCTTC 61723
QY 481 TTACTGTCCCTTCTGGGCTCAGTATGCTGCGCCGCCAGTGGGACTTTGGAATCAATGT 540
Db 61724 TTACTGTCCCTTCTGGGCTCAGTATGCTGCGCCGCCAGTGGGACTTTGGAATCAATGT 61783
QY 541 GTCAACTCTTTGACAGGCTCTAATTTATAGGCTTCTCTCTGGAATCTTCTTCATCACTC 600
Db 61784 GTCAACTCTTTGACAGGCTCTAATTTATAGGCTTCTCTCTGGAATCTTCTTCATCACTC 61843
QY 601 TCTTGACAATCATGATAGTACCTGGCTGTGCTCCATCTCTGTGTGTGTGTGTGTGTGTGTGT 660
Db 61844 TCTTGACAATCATGATAGTACCTGGCTGTGCTCCATCTCTGTGTGTGTGTGTGTGTGTGTGT 61903
QY 661 CGGTCACTTTGGGCTGGTGAAGTGTGATCAGTGGGTGGGTGGGTGGGTGGGTGGGTGGT 720
Db 61904 CGGTCACTTTGGGCTGGTGAAGTGTGATCAGTGGGTGGGTGGGTGGGTGGGTGGGTGGT 61963
QY 721 TCCAGGAATCATCTTTTACCAGATCTCAAAAGAGAGGTCTTCAATACACCTGCAAGTCTC 780
Db 61964 TCCAGGAATCATCTTTTACCAGATCTCAAAAGAGAGGTCTTCAATACACCTGCAAGTCTC 62023
QY 781 ATTTCATCAT-----ACATTAAAGATAGTCACT 808
Db 62024 ATTTCATCATCATGATCAATTTCTGGAAGAAATTTCCAGACATTAAGATAGTCACT 62083

Matches 1432; Conservative 0; Mismatches 3; Indels 35; Gaps 2;

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QY 1 GAATCCCCACAGAGCCAAAGCTCCCATCTAGTGGACAGGAAGCTAGCAGCAACCT 60
Db 61244 GAATCCCCACAGAGCCAAAGCTCCCATCTAGTGGACAGGAAGCTAGCAGCAACCT 61303
QY 61 TCCTTCCTACAGCAAACTCATGCTTGCCCAAAAAGAGAGTAATTCATGTAGACATC 120
Db 61304 TCCTTCCTACAGCAAACTCATGCTTGCCCAAAAAGAGAGTAATTCATGTAGACATC 61363
QY 121 TATGTAGCAATATAAACCTATTGATGTATATAACAGTTGCAATTCATGAGGGCAACT 180
Db 61364 TATGTAGCAATATAAACCTATTGATGTATATAACAGTTGCAATTCATGAGGGCAACT 61423
QY 181 AATATATCTAGACATTTATAAAGATCACTTTTATTTATGTCACAGGTTGGAACAAGA 240
Db 61424 AATATATCTAGACATTTATAAAGATCACTTTTATTTATGTCACAGGTTGGAACAAGA 61483
QY 241 TGGATTATCAAGTGTCAAGTCCAACTATGACATCAATATTATATCATCGGCGCCTGCC 300
Db 61484 TGGATTATCAAGTGTCAAGTCCAACTATGACATCAATATTATATCATCGGCGCCTGCC 61543
QY 301 AAAAAATCAATGTGAAGCAAAATCGCAGCCGCTCCCTGCTCCGCTCTACTCACTGGTGT 360
Db 61544 AAAAAATCAATGTGAAGCAAAATCGCAGCCGCTCCCTGCTCCGCTCTACTCACTGGTGT 61603
QY 361 TCATCTTTGGTTTGTGGGCACATGCTGGTTCATCTCATCTCTGATTAACATGCAAAAGGC 420
Db 61604 TCATCTTTGGTTTGTGGGCACATGCTGGTTCATCTCATCTCTGATTAACATGCAAAAGGC 61663
QY 421 TGAAGAGCATGACATGACATCTACCTGCTCAACCTGGCCATCTCTGACCTGTTTTTCTTC 480
Db 61664 TGAAGAGCATGACATGACATCTACCTGCTCAACCTGGCCATCTCTGACCTGTTTTTCTTC 61723
QY 481 TTACTGTCCCTCTGGGCTCACTATGCTGCGGCCAGTGGGACATTTGGAAATACAAATGT 540
Db 61724 TTACTGTCCCTCTGGGCTCACTATGCTGCGGCCAGTGGGACATTTGGAAATACAAATGT 61783
QY 541 GTCAACTCTTGACAGGCTCTATTTTATAGGCTTCTTCTGGAATCTTCTCATATCC 500
Db 61784 GTCAACTCTTGACAGGCTCTATTTTATAGGCTTCTTCTGGAATCTTCTCATATCC 61843
QY 601 TCCTGACAACTAGTAGTACCTGGCTGCTGCCATCTGCTGTTGTTGCTTTAAAGCCAGGA 660
Db 61844 TCCTGACAACTAGTAGTACCTGGCTGCTGCCATCTGCTGTTGTTGCTTTAAAGCCAGGA 61903
QY 661 CGGTACCTTTGGGTTGGTGACAAGTGTGATCACTTGGGTTGGTGTGCTGTTGGCTCTC 720
Db 61904 CGGTACCTTTGGGTTGGTGACAAGTGTGATCACTTGGGTTGGTGTGCTGTTGGCTCTC 61963
QY 721 TCCGAGGAATCATCTTTACAGATCTCAAAAAGAGTCTTCAATACACCTGCGAGCTCTC 780
Db 61964 TCCGAGGAATCATCTTTACAGATCTCAAAAAGAGTCTTCAATACACCTGCGAGCTCTC 62023
QY 781 ATTTTCCAT-----ACATTAAGATAGTCACT 808
Db 62024 ATTTTCCATACAGTCAGTATCAATCTGGAAGAAATTCAGACATTAAGAATAGTCACT 62083
QY 809 TGGGCTGTGCTGCTGCCCTGCTGTCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 868
Db 62084 TGGGCTGTGCTGCTGCCCTGCTGTCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 62143
QY 869 TGCTTGGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 928
Db 62144 TGCTTGGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 62203
QY 929 TGAATGTTATTTTCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 988
Db 62204 TGAATGTTATTTTCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 62263
QY 989 AGGAATCTTTGGCTGAAATTAATGAGTAGTCTTAACAGTTGGACCAAGCTATGACAG 1048
Db 62264 AGGAATCTTTGGCTGAAATTAATGAGTAGTCTTAACAGTTGGACCAAGCTATGACAG 62323
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QY 1049 TGACAGAGACTCTTGGATGAGGCACTGCTGATCAACCCCATCATCTATGCTTTGTG 1108
Db 62324 TGACAGAGACTCTTGGATGAGGCACTGCTGATCAACCCCATCATCTATGCTTTGTG 62383
QY 1109 GGGAGAGTTTCAGAACTACCTCTTAGTCTTCTTCCAAAGCAGCATGCGAAAGCTTCT 1168
Db 62384 GGGAGAGTTTCAGAACTACCTCTTAGTCTTCTTCCAAAGCAGCATGCGAAAGCTTCT 62443
QY 1169 GCAATATCTCTTCTATTTTCCAGCAAGAGCTCCCGAGCGAGCAAGCTCAGTTTACACC 1228
Db 62444 GCAATATCTCTTCTATTTTCCAGCAAGAGCTCCCGAGCGAGCAAGCTCAGTTTACACC 62503
QY 1229 GATCCACTGGGAGCAGGAAATATCTGTGGGCTTGTGACAGGACTCAAGTGGGCTGGT 1288
Db 62504 GATCCACTGGGAGCAGGAAATATCTGTGGGCTTGTGACAGGACTCAAGTGGGCTGGT 62563
QY 1289 ACCCAGTCACAGTTGTGCACATGCTTACTGTTTATAGAGGCTTAAGATTCACTCAATT 1346
Db 62564 ACCCAGTCACAGTTGTGCACATGCTTACTGTTTATAGAGGCTTAAGATTCACTCAATT 62623
QY 1347 -TTGGGAGGCTTTTAAAGAGGAGTACTGTTTATAGAGGCTTAAGATTCACTCAATT 1405
Db 62624 TGGGAGAGGCTTTTAAAGAGGAGTACTGTTTATAGAGGCTTAAGATTCACTCAATT 62683
QY 1406 ATTTGGCATCTGTTTAAAGTAGATTAGATC 1435
Db 62684 ATTTGGCATCTGTTTAAAGTAGATTAGATC 62713
```

RESULT 9

AAA35151

ID AAA35151 standard; DNA; 149412 BP.

XX AC AAA35151;

XX DT 28-JUL-2000 (first entry)

XX DE Human adenosine receptor related polynucleotide 2nd SEQ ID NO:25.

Human; adenosine receptor; low adenosine antisense oligonucleotide; phosphorothioate; impaired respiration; inflammation; allergy; allergic disease; bronchoconstriction; inhibitor; antiinflammatory; antiallergic; antisthmatic; cytostatic; analgesic; impaired airway; lung disease; ischaemic condition; pulmonary vasoconstriction; asthma; respiratory distress syndrome; pain; cystic fibrosis; emphysema; pulmonary hypertension; chronic obstructive pulmonary disease; COPD; cancer; leukaemia; lymphoma; carcinoma; metastasis; ss.

XX OS Homo sapiens.

XX PN W0200009525-A2.

XX PD 24-FEB-2000.

XX PF 03-AUG-1999; 99WO-US17712.

XX PR 03-AUG-1998; 98US-0095212.

XX PA (UYEC-) UNIV EAST CAROLINA.

XX PI Nyce JW;

XX DR WPI; 2000-205971/18.

XX PT New antisense oligonucleotides useful for treating e.g. pulmonary vasoconstriction, inflammation, allergies, asthma, hypertension, bronchitis, emphysema, respiratory distress syndrome, ischemia or cancers

XX PS Disclosure; Page 1138-1171; 1343pp; English.

XX CC The present invention describes a new composition comprising an

KW	respiratory obstruction; pulmonary obstruction; impeded respiration;
KW	surfactant hypoproduction; pulmonary vasoconstriction; asthma; RDS;
KW	respiratory distress syndrome; pain; cystic fibrosis; allergic rhinitis;
KW	pulmonary hypertension; emphysema; pulmonary transplantation rejection;
KW	chronic obstructive pulmonary disease; pulmonary infection; bronchitis;
KW	cancer; ss.

XX	Homo sapiens.
OS	

XX
PN
WO200062736-A2XX
PD 26-007-3000

XX
24 000 000 000 000 000 000

XX

ER 00-APR-1999; 9905-012/938
XX

PA (UYEC-) UNIV EAST
PA (NYCE/) NYCE J W.

XX
PI
Nyce JW;XX
DR
WPT: 2000-679539/66

xx Low adenosine (A) content antisense oligonucleotides which do not
pt trigger adenosine receptors during metabolism, useful e.g. for treating
pt cancers and respiratory obstructions -

XX
PS
Disclosure: Page 1219-1254: 1592pp: English.

The present invention describes low adenosine (A) content antisense oligonucleotides and compositions (I) comprising them. In the antisense oligonucleotides the A is replaced by a 'universal' or alternative base. (I) can have respiratory, bronchodilator, antiinflammatory, analgesic, immunosuppressive, antiasthmatic, hypotensive and cytostatic activities. The antisense oligonucleotides and (I) can be used to down-regulate the expression and/or activity of target polypeptides associated with lung/respiratory disorders and malignancies, such as stimulating and activating peptide factors and transmitters, transcription factors, immunoglobulins and antibodies, antibody receptors, cytokines and chemokines, endogenously produced specific and non-specific enzymes, binding proteins, adhesion molecules and their receptors, cytokine and chemokine receptors, adenosine receptors, bradykinin receptors, central nervous system (CNS) and peripheral nervous and non-nervous system receptors, CNS and peripheral nervous and non-nervous system peptide transmitters, defensins, growth factors, vasoactive peptides and receptors, binding proteins and malignancy associated proteins. The antisense oligonucleotides may be used in this way to treat disorders including respiratory obstruction (especially pulmonary obstruction and/or bronchoconstriction) and/or lung inflammation, allergy(ies) and/or selected hypoproduction which are associated with a disease or condition selected from pulmonary vasoconstriction, inflammation, allergies, asthma, impeded respiration, respiratory distress syndrome (RDS), pain, cystic fibrosis (CF), allergic rhinitis (AR), pulmonary hypertension, emphysema, chronic obstructive pulmonary disease (COPD), pulmonary transplantation rejection, pulmonary infections, bronchitis, and/or cancer. AAF18434 to AAF21543 represent human polynucleotide fragments and antisense oligonucleotides used in the exemplification of the present invention.

XX SO Semence 152740 BP: 44169 A: 32023 C: 34549 C: 41999 T: 0 other:

Query Match 95.4%; Score 1375.2; DB 21; Length 152740;
Best Local Similarity 97.4%; Pred. No. 0;
Matches 1432; Conservative 0; Mismatches 3; Indels 35; Gaps 2;

09 1 GAATTCGGCCACAGAGGCCAAGGCTCTGCATCTACTGTGGACAGGGGAAGCTAGCAGCAAAACCT 60

[illegible]

Country	Year	Value
Algeria	1990	0.00
Algeria	1991	0.00
Algeria	1992	0.00
Algeria	1993	0.00
Algeria	1994	0.00
Algeria	1995	0.00
Algeria	1996	0.00
Algeria	1997	0.00
Algeria	1998	0.00
Algeria	1999	0.00
Algeria	2000	0.00
Algeria	2001	0.00
Algeria	2002	0.00
Algeria	2003	0.00
Algeria	2004	0.00
Algeria	2005	0.00
Algeria	2006	0.00
Algeria	2007	0.00
Algeria	2008	0.00
Algeria	2009	0.00
Algeria	2010	0.00
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Algeria	2014	0.00
Algeria	2015	0.00
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Algeria	2027	0.00
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Algeria	2036	0.00
Algeria	2037	0.00
Algeria	2038	0.00
Algeria	2039	0.00
Algeria	2040	0.00
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Algeria	2043	0.00
Algeria	2044	0.00
Algeria	2045	0.00
Algeria	2046	0.00
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Algeria	2064	0.00
Algeria	2065	0.00
Algeria	2066	0.00
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Algeria	2069	0.00
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Algeria	2080	0.00
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Algeria	2085	0.00
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Algeria	2087	0.00
Algeria	2088	0.00
Algeria	2089	0.00
Algeria	2090	0.00
Algeria	2091	0.00
Algeria	2092	0.00
Algeria	2093	0.00
Algeria	2094	0.00
Algeria	2095	0.00
Algeria	2096	0.00
Algeria	2097	0.00
Algeria	2098	0.00
Algeria	2099	0.00
Algeria	2100	0.00
Algeria	2101	0.00
Algeria	2102	0.00
Algeria	2103	0.00
Algeria	2104	0.00
Algeria	2105	0.00
Algeria	2106	0.00
Algeria	2107	0.00
Algeria	2108	0.00
Algeria	2109	0.00
Algeria	2110	0.00
Algeria	2111	0.00
Algeria	2112	0.00
Algeria	2113	0.00
Algeria	2114	0.00
Algeria	2115	0.00
Algeria	2116	0.00
Algeria	2117	0.00
Algeria	2118	0.00
Algeria	2119	0.00
Algeria	2120	0

[illegible]

QY	121	TATGTAGGCAATTTAAACCTATTGATGTATAAACAGTTTGATTAATCAAGGAGGCAACT	180
Db	67708	TATGTAGGCAATTTAAACCTATTGATGTATAAACAGTTTGATTAATCAAGGAGGCAACT	67767
QY	181	AAATACATCTTAGGACTTTATAAAGATCACATTTTTATTATGACAGGGTGAACAAGA	240
Db	67768	AAATACATCTTAGGACTTTATAAAGATCACATTTTTATTATGACAGGGTGAACAAGA	67827
QY	241	TGGATTACAAGTGCAAGTCCAATCTATGACATCAATATTATTATACATCGGAGCCCTGCC	300
Db	67828	TGGATTACAAGTGCAAGTCCAATCTATGACATCAATATTATTATACATCGGAGCCCTGCC	67887
QY	301	AAAAAATCAATGTGAAGCAATCGCAGCCGCGCTTCGCTCGGCTCTACTCACTGGTGT	360
Db	67888	AAAAAATCAATGTGAAGCAATCGCAGCCGCGCTTCGCTCGGCTCTACTCACTGGTGT	67947
QY	361	TCATCTTTGGTTTTGTGGCAACATCGTGGTCACTCCCTCACTGTAACTGACAAAGGC	420
Db	67948	TCATCTTTGGTTTTGTGGCAACATCGTGGTCACTCCCTCACTGTAACTGACAAAGGC	68007
QY	421	TGAAGAGCATGACTGACATCTACCTGCTCAACCTGGCCATCTCTGACCTGTTTTCTCTC	480
Db	68008	TGAAGAGCATGACTGACATCTACCTGCTCAACCTGGCCATCTCTGACCTGTTTTCTCTC	68067
QY	481	TTACTGTCCCTTCCTGGGCTCACATGCTGTGGCGCCAGTGGGACTTTGGAAATACATGT	540
Db	68068	TTACTGTCCCTTCCTGGGCTCACATGCTGTGGCGCCAGTGGGACTTTGGAAATACATGT	68127
QY	541	GTCAACTCTTGACAGGGCTCTATTTTTATAGGCTTCTTCTCTGGAATCTCTTCATCATCC	600
Db	68128	GTCAACTCTTGACAGGGCTCTATTTTTATAGGCTTCTTCTCTGGAATCTCTTCATCATCC	68187
QY	601	TCCTGTCAATCATGATAGGTACTCGCTGCTGCCTCATCTGTGTTGCTTTAAAGCCAGGA	660
Db	68188	TCCGTGCAATCATGATAGGTACTCGCTGCTGCCTCATCTGTGTTGCTTTAAAGCCAGGA	68247
QY	661	CGGTCACCTTTGGGTGGTGACAAGTGTGATCACTTGGGTGGGTGTGTTTGCCTCTC	720
Db	68248	CGGTCACCTTTGGGTGGTGACAAGTGTGATCACTTGGGTGGGTGTGTTTGCCTCTC	68307
QY	721	TCCCAGGATCATCTTTACAGATCTCTCAAAAGAGGCTCTTCAATACACCTTGCAGCTCTC	780
Db	68308	TCCCAGGAATCATCTTTACAGATCTCTCAAAAGAGGCTCTTCAATACACCTTGCAGCTCTC	68367
QY	781	ATTTTTCAT-----ACATTAAGATAGTCACT	808
Db	68368	ATTTTTCATACAGTCAGTATCAATTTCTGGAAGATTTCCAGACATTTAAAGATGTCATCT	68427
QY	809	TGGGGCTGGTCTGGCGTGGTGTCTATGGTCATCTGCTACTCGGGAATCTTAAAACTC	868
Db	68428	TGGGGCTGGTCTGGCGTGGTGTCTATGGTCATCTGCTACTCGGGAATCTTAAAACTC	68487
QY	869	TGCTTCGGTGTGGAATGAGAAGACAGGACAGGGCTGTGAGGCTTATCTTCAACATCA	928
Db	68488	TGCTTCGGTGTGGAATGAGAAGACAGGACAGGCGTGTGAGGCTTATCTTCAACATCA	68547
QY	929	TGATTTGTTATTTTCTCTCTGGGCTCCCTAGACATTTGCTCTTCTCTGAAACCTCTC	988
Db	68548	TGATTTGTTATTTTCTCTCTGGGCTCCCTAGACATTTGCTCTTCTCTGAAACCTCTC	68607
QY	989	AGGAATCTTTGGCTGGAATAATTTGACGTAGTCTTAACAGTTTGGACCAAGTATGAGG	1048
Db	68608	AGGAATCTTTGGCTGGAATAATTTGACGTAGTCTTAACAGTTTGGACCAAGTATGAGG	68667
QY	1049	TGACAGAGACTCTTGGGATGAGCACTGCTGCATCAACCCCATCATCTATGCCTTTGTG	1108
Db	68668	TGACAGAGACTCTTGGGATGAGCACTGCTGCATCAACCCCATCATCTATGCCTTTGTG	68727
QY	1109	GGGAGAGTTTCAGAACTTACCTCTTAGTCTTCTTCCAAAAGACATTTGCCAAAGCTTCT	1168
Db	68728	GGGAGAGTTTCAGAACTTACCTCTTAGTCTTCTTCCAAAAGACATTTGCCAAAGCTTCT	68787

QY 1169 GCAAAAGCTGTTTATTTTCCAGCAGAGAGGCTCCCGAGCGAGCAAGCTCAGTTTACACC 1288
DB 68788 GCAAAAGCTGTTTATTTTCCAGCAGAGAGGCTCCCGAGCGAGCAAGCTCAGTTTACACC 68847
QY 1229 GATCCACTGGGAGCAGGAAATATCTGTGGGCTTGTGACAGGACTCAAGTGGCTGGTG 1288
DB 68848 GATCCACTGGGAGCAGGAAATATCTGTGGGCTTGTGACAGGACTCAAGTGGCTGGTG 68907
QY 1289 ACCAGTCAGAGTGTGTCACATGCTAGTTTTCATACACAGCCCTGGCTGGGCTGGTG-- 1346
DB 68908 ACCAGTCAGAGTGTGTCACATGCTAGTTTTCATACACAGCCCTGGCTGGGCTGGTG 68967
QY 1347 -TTGGAGGCTGTTTAAAGGAGGTTACTGTTATAGAGGCTTAGATTCATCCATT 1405
DB 68968 TGGGAGAGGCTGTTTAAAGGAGGTTACTGTTATAGAGGCTTAGATTCATCCATT 69027
QY 1406 ATTGGCATCTGTTTAAAGTAGATTAGATC 1435
DB 69028 ATTGGCATCTGTTTAAAGTAGATTAGATC 69057
RESULT 11
AAA34983
ID AAA34983 standard; DNA; 143068 BP.
AC AAA34983;
XX
DT 28-JUL-2000 (first entry)
XX
DE Human adenosine receptor related polynucleotide SEQ ID NO:2672.
KW Human; adenosine receptor; low adenosine antisense oligonucleotide;
KW phosphothioate; impaired respiration; inflammation; allergy;
KW allergic disease; bronchoconstriction; inhibitor; antiinflammatory;
KW antiallergic; antiasthmatic; cytotatic; analgesic; impaired airway;
KW lung disease; ischemic condition; pulmonary vasoconstriction; asthma;
KW respiratory distress syndrome; pain; cystic fibrosis; emphysema;
KW pulmonary hypertension; chronic obstructive pulmonary disease; COPD;
KW cancer; leukaemia; lymphoma; carcinoma; metastasis; ss.
XX Homo sapiens.
OS
XX WO200009525-A2.
PN
XX 24-FEB-2000.
PD
XX 03-AUG-1999; 99WO-US17712.
PF
XX 03-AUG-1998; 98US-0095212.
PR
XX (UYEC-) UNIV EAST CAROLINA.
PA
XX NYce JW;
PI
XX WPI; 2000-205971/18.
DR
XX
XX New antisense oligonucleotides useful for treating e.g. pulmonary
PT vasoconstriction, inflammation, allergies, asthma, hypertension
PT bronchitis, emphysema, respiratory distress syndrome, ischemia or
PT cancers -
XX
XX Disclosure; Page 851-882; 1343pp; English.
PS
XX The present invention describes a new composition comprising an
CC antisense oligonucleotide (ON) with low adenosine (up to 15%), which
CC targets nucleic acids involved in bronchoconstriction, allergies, and/or
CC inflammation. The ON can have antiinflammatory, antiallergic,
CC antiasthmatic, cytostatic and analgesic activities. The compositions are
CC useful for the treatment of diseases associated with inflammation,
CC impaired airways, including lung disease and diseases whose secondary
CC effects afflict the lungs of a subject. They can be used for treating
CC e.g. ischemic conditions, pulmonary vasoconstriction, allergies,
CC asthma, impeded respiration, respiratory distress syndrome, pain, cystic

CC fibrosis, pulmonary hypertension, emphysema, chronic obstructive
CC pulmonary disease (COPD), and cancers such as leukemias, lymphomas,
CC carcinomas, and cancers which may metastasize to the lungs, including
CC breast and prostate cancer. The reduction of the adenosine content of
CC the ONs reduces side effects. The A-containing ONs break down with the
CC release of deoxyadenosine which activates adenosine receptors causing
CC bronchoconstriction and inflammation. AAA32313 to AAA35312 represent the
CC nucleotide sequences given in the sequence listing from the present
CC invention, which correspond to SEQ ID NO:1 to 2815, and then the last
CC 185 sequences are also called SEQ ID NO:1 to 185, but the sequences
CC differ from the previously named sequences. SEQ ID NO:11 to 1680
CC (AAA32323 to AAA33992) are specifically claimed ONs from the present
CC invention. N.B. Sequences given in the disclosure of the present
CC invention do not match up with their corresponding SEQ ID NO: sequences
CC given in the sequence listing.
XX
SQ Sequence 143068 BP; 41194 A; 30122 C; 32402 G; 39350 T; 0 other;
Query Match 95.38; Score 1373.6; DB 21; Length 143068;
Best local Similarity 97.34; Pred. No. 0;
Matches 1431; Conservative 0; Mismatches 4; Indels 35; Gaps 2;
QY 1 GAATTCCTCCCAACAGAGCCCAAGCTCTCCATCTAGTGACAGGAGGCTAGCAGCAAACT 60
DB 61244 GAATTCCTCCCAACAGAGCCCAAGCTCTCCATCTAGTGACAGGAGGCTAGCAGCAAACT 61303
QY 61 TCCCTTCACTACAAACTTCATCTGCTTGGCCAAAAGAGAGTTAATCAATGTAGACATC 120
DB 61304 TCCCTTCACTACAAACTTCATCTGCTTGGCCAAAAGAGAGTTAATCAATGTAGACATC 61363
QY 121 TATGTAGGCAATATAAACCCTATGATGTATAAACAAGTTTGCATTCATGGAGGCACT 180
DB 61364 TATGTAGGCAATATAAACCCTATGATGTATAAACAAGTTTGCATTCATGGAGGCACT 61423
QY 181 AATATCACTTAGGACCTTTATAAAGATCACTTTTATTATGACAGAGGTGGAACAAGA 240
DB 61424 AATATCACTTAGGACCTTTATAAAGATCACTTTTATTATGACAGAGGTGGAACAAGA 61483
QY 241 TGGATTATCAAGTCAAGTCCCAATCTATGACATCAATATTATATACATCGAGCCCTGCC 300
DB 61484 TGGATTATCAAGTCAAGTCCCAATCTATGACATCAATATTATATACATCGAGCCCTGCC 61543
QY 301 AAAAAATCAATGTGAAGCAAAATCGCAGCCGCCCTCCCTGCTCCGCTCTACTCTGCTGT 360
DB 61544 AAAAAATCAATGTGAAGCAAAATCGCAGCCGCCCTCCCTGCTCCGCTCTACTCTGCTGT 61603
QY 361 TCATCTTTGGTTTGTGGGCAACATGCTGGTCACTCCTCATCTCATCACTGCAAAAGGC 420
DB 61604 TCATCTTTGGTTTGTGGGCAACATGCTGGTCACTCCTCATCTCATCACTGCAAAAGGC 61663
QY 421 TGAAGAGCATGACTGACATCTACCTGCTCAACCTGGCCATCTCTGACCTGTTTTCCTTC 480
DB 61664 TGAAGAGCATGACTGACATCTACCTGCTCAACCTGGCCATCTCTGACCTGTTTTCCTTC 61723
QY 481 TTACTGCTCCCTTCTGGGCTCACTATGCTGCGCCGAGCTGGGACTTTGGAATACAAATGT 540
DB 61724 TTACTGCTCCCTTCTGGGCTCACTATGCTGCGCCGAGCTGGGACTTTGGAATACAAATGT 61783
QY 541 GTCACCTCTTGACAGGCTCTAATTTATAGGCTTTCTCTCGAATCTCTCATCATCC 600
DB 61784 GTCACCTCTTGACAGGCTCTAATTTATAGGCTTTCTCTCGAATCTCTCATCATCC 61843
QY 601 TCTGACATGCTAGTACCTGGCTGCTGCCATCTGCTGTTTGTCTTAAAGCCAGGA 660
DB 61844 TCTGACATGCTAGTACCTGGCTGCTGCCATCTGCTGTTTGTCTTAAAGCCAGGA 61903
QY 661 CGGTCACTTTGGGCTGGTGACAAAGTGTGATCACTTTGGGCTGGCTGTTTTCCTTC 720
DB 61904 CGGTCACTTTGGGCTGGTGACAAAGTGTGATCACTTTGGGCTGGCTGTTTTCCTTC 61963
QY 721 TCCAGGAATCATCTTTACAGATCTCAAAAAGAGGTCTTCATTTACACCTGACGCTTC 780
DB 61964 TCCAGGAATCATCTTTACAGATCTCAAAAAGAGGTCTTCATTTACACCTGACGCTTC 62023

QY 481 TTACTGTCCCTTCCTGGGCTCACTATGCTGCCGCCAGTGGGACTTTGGAAATACAAATGT 540
DB 481 TTACTGTCCCTTCCTGGGCTCACTATGCTGCCGCCAGTGGGACTTTGGAAATACAAATGT 540
QY 541 GTCAACTCTTGACAGGCTCTATTTATAGGCTCTCTCTGAAATCTTCTCATCATCC 600
DB 541 GTCAACTCTTGACAGGCTCTATTTATAGGCTCTCTCTGAAATCTTCTCATCATCC 600
QY 601 TCTGCAATCGATAGGTACCTGGCTGCTGCTCCATGCTGTGTTGCTTTAAAGCCAGGA 660
DB 601 TCTGCAATCGATAGGTACCTGGCTGCTGCTCCATGCTGTGTTGCTTTAAAGCCAGGA 660
QY 661 CGGTCACTTTGGGCTGGTGAAGTGTGATCATCTGGGTGGTGGTGTGTTGCTGCTC 720
DB 661 CGGTCACTTTGGGCTGGTGAAGTGTGATCATCTGGGTGGTGGTGTGTTGCTGCTC 720
QY 721 TCCAGGATCATCTTTACAGATCTCAAAAGAGGCTCTCATACAGCTGAGCTCTC 780
DB 721 TCCAGGATCATCTTTACAGATCTCAAAAGAGGCTCTCATACAGCTGAGCTCTC 780
QY 781 ATTTTCATACATTAAGATAGTATCTTTGGGCTGCTGCTGCTGCTGCTGCTGCTGCT 840
DB 781 ATTTTCATACATTAAGATAGTATCTTTGGGCTGCTGCTGCTGCTGCTGCTGCTGCT 840
QY 841 ATCTGCTTCTCGGAACTCTAAAGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 900
DB 841 ATCTGCTTCTCGGAACTCTAAAGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 900
QY 901 AGGCTGTGAGGCTTATCTTCAACATCATGATTTTATTTCTCTCTGCTGCTGCTGCT 960
DB 901 AGGCTGTGAGGCTTATCTTCAACATCATGATTTTATTTCTCTCTGCTGCTGCTGCT 960
QY 961 AACATGCTCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1020
DB 961 AACATGCTCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1020
QY 1021 TCTAACAGGTTGGACCAAGCTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1080
DB 1021 TCTAACAGGTTGGACCAAGCTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1080
QY 1081 ATCAACCCATCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1140
DB 1081 ATCAACCCATCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1140
QY 1141 TTCCAAAGCAGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1200
DB 1141 TTCCAAAGCAGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1200
QY 1201 CCGAGGAGCAGGCTCAGTTTACCCGATCCACTGGGAGCAGGAAATATCTGTGGG 1260
DB 1201 CCGAGGAGCAGGCTCAGTTTACCCGATCCACTGGGAGCAGGAAATATCTGTGGG 1260
QY 1261 TTGTGACAGGACTCAAGTGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1320
DB 1261 TTGTGACAGGACTCAAGTGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1320
QY 1321 TCATACACAGCTGGGCTGGGGT 1344
DB 1321 TCATACACAGCTGGGCTGGGGT 1344

RESULT 13
ID AAH26903
XX
AC AAH26903;
XX
DT 21-DEC-2001 (first entry)
XX
DE Human HIV-1 co-receptor CCR5 nucleotide sequence.
XX
KW CCR5; chemokine; co-receptor; human immunodeficiency virus type 1;

KW HIV-1; infection; therapy; vaccine; anti-HIV-1; ss.
XX Homo sapiens.
OS
XX
FH Key Location/Qualifiers
FT CDS 240..1298
XX /*cag= a
PN WO200164710-A2.
PD
XX 07-SEP-2001.
XX 28-FEB-2001; 2001WO-US06699.
XX 29-FEB-2000; 2000US-185667P.
PR 19-MAY-2000; 2000US-205839P.
PR 07-FEB-2001; 2001US-267231P.
XX (PROG-) PROGENICS PHARM INC.
PA (AARO-) AARON DIAMOND AIDS RES CENT.
XX
PI Dragic T, Olson WC;
XX
XX WPI; 2001-611273/70.
DR P-PSDB; AAB82948.
XX
XX Novel compounds comprising specific amino acids within CCR5 (HIV 1
PT co-receptor) amino terminal domain including negatively charged and two
PT sulfated tyrosine residues is useful for treating HIV infection in
XX humans
PS Disclosure; Page 30-31; 163pp; English.
XX
CC The present sequence is that of a polynucleotide encoding the
CC human HIV-1 co-receptor CCR5 (see AAB82948). Amino acids 2-18
CC in the N-terminal region of CCR5 comprise an HIV gp120-binding
CC site that determines the specificity of the interaction between
CC CCR5 and gp120. Post-translational sulfation of the tyrosine
CC residues in the CCR5 N-terminus is required for gp120 binding and
CC may critically modulate the susceptibility of target cells to HIV-1
CC infection in vivo. The invention provides claimed sulfated
CC peptides (see AAB82947) that are based on the CCR5 N-terminal
CC region and which are effective for inhibiting HIV-1 binding to
CC CCR5. These peptides are used in claimed methods of inhibiting HIV
CC infection of CD4+ cells, of preventing CD4+ cells from becoming
CC infected with HIV, of treating a subject whose CD4+ cells are
CC infected with HIV, and of identifying an agent which inhibits
CC binding of a CCR5 ligand to a CCR5 receptor. The methods may be
CC carried out in a subject, especially a human, infected (therapeutic
CC method), not infected with HIV (prophylactic method), or in a
CC subject who is not infected with, but has been exposed to, HIV.
XX
SQ Sequence 1376 BP; 347 A; 338 C; 297 G; 394 T; 0 other;
Query Match 90.3%; Score 1302; DB 22; Length 1376;
Best Local Similarity 97.7%; Pred. No. 0;
Matches 1344; Conservative 0; Mismatches 0; Indels 32; Gaps 1;
QY 1 GAATTCCTCCCAACAGAGCCAGCTCTCCATCTAGTGGACAGGGAAGCTAGCAGCAACCT 60
DB 1 GAATTCCTCCCAACAGAGCCAGCTCTCCATCTAGTGGACAGGGAAGCTAGCAGCAACCT 60
QY 61 TCCCTTCACTACAAAACCTCAATTCCTTGGCCAAAAGAGAGTTAATTCATGTAGACATC 120
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QY 121 TATGTAGCAATTTAAACACCTATTGATGTATATAACAGTTTGCATTTCATGGAGGCAACT 180
DB 121 TATGTAGCAATTTAAACACCTATTGATGTATATAACAGTTTGCATTTCATGGAGGCAACT 180
QY 181 AAATACATCTTAGGACTTTATAAAGATCACTTTTATTATGCACAGGGTGGAAACAAGA 240
DB 181 AAATACATCTTAGGACTTTATAAAGATCACTTTTATTATGCACAGGGTGGAAACAAGA 240

QY	1	GAATTCCCCACAGAGCCAGCTCTCCATCTAGTGTGGACAGGAGCTAGCAGCAAACT	60
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QY	61	TCCCTTCACATACAAAACCTTCATTGCTTGTCGCAAAAGAGAGTTAATTCATGTAGACATC	120
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QY	121	TATGTAGSCAAATTAATAAACCTTATGTATATATAAACAGTTTGCAATTCATGAGGSCAACT	180
Db	121		
QY	181	AAATACATCTAGGACTTATAAAGATCACTTTTATTTATGSCACAGGCTGGAACAGA	240
Db	181		
QY	241	TGGATTATCAAGTGTCAAGTCCAACTATGACATCAATATTATACATCGGAGCCCTGCC	300
Db	241		
QY	301	AAAAATCAATGTGAAGCAAAATCGAGCCCGCTCTGCTCCGCTCTACTCAGCTGGTGT	360
Db	301		
QY	361	TCATCTTTGGTTTGTGGGCAACATGCTGGTCATCTCTGATATAAATGCAAAAGGC	420
Db	361		
QY	421	TGAGAGCATGACTGACATCTACTGCTCTCAACCTGGGCATCTCTGACCTGTTTCCCTTC	480
Db	421		
QY	481	TTACTGTCCCTTCTGGGCTCACCTATGCTGGCGCCAGTGGGACTTTTGGAAATACAATGT	540
Db	481		
QY	541	GTCAACTCTTGACAGGGCTCTATTATATAGGCTTCTCTGTGSAATCTTCTTCATCATCC	600
Db	541		
QY	601	TCCTGACAATCGATAGTACTGGCTGTGTCCTCATGCTGTTCCTTTAAAGACGAGGA	660
Db	601		
QY	661	CGGTACACCTTTGGGCTGTGCAAGTGTGATCACTTGGGTGGCTGTGTTGGCTCTC	720
Db	661		
QY	721	TCCAGGAATCACTTTACAGATCTCAAAAGAGGCTCTTCATTACACCTGCAGCTCTC	780
Db	721		
QY	781	ATTTTCCAT-----ACATTTAAGATAGTCATCT	808
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QY	809	TGGGCTGGCTCGCGCTGCTGTCTATGGTGCATCTGCTACTCGGGAACTCTAAAACCTC	868
Db	841	TGGGGCTGGCTCGCGCTGCTGTCTATGGTGCATCTGCTACTCGGGAACTCTAAAACCTC	900
QY	869	TGCTTCGGTGTGAAATAGAGAAGAGGACAGGGCTGTGAGGCTTATCTTCACCATCA	928
Db	901	TGCTTCGGTGTGAAATAGAGAAGAGGACAGGGCTGTGAGGCTTATCTTCACCATCA	960
QY	929	TGATTGTATTTTCTTCGTGGGCTCCCTTACAACTATGCTTCTCTGAAACCTTCC	988
Db	961	TGATTGTATTTTCTTCGTGGGCTCCCTTACAACTATGCTTCTCTGAAACCTTCC	1020
QY	989	AGAAATCTTTGGCTGGAATAATTGCAAGTAGCTCTTAACAGGTTGGACCAAGCTATGCAGG	1048
Db	1021	AGAAATCTTTGGCTGGAATAATTGCAAGTAGCTCTTAACAGGTTGGACCAAGCTATGCAGG	1080
QY	1049	TGACAGAGACTCTTGGGATGACGCACTGCTGCATCAACCCCATCATCTATGCTTTGCTG	1108

RESUME 15

RESOL 13
A2F26390

AAE26390 standard: 1414 BP.

XX AAF26390:

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'06C07JMY

DT 04-MAY-2001 (first entry)

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DE Human HDG NR10 cDNA.

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KW HDGNR10; G-protein chemokine receptor; antiinflammatory; vulnery;

KW immunomodulatory; anticoagulant; antiallergic; immunosuppressive; human; human

[illegible]

vasotropic; gene therapy; haematopoiesis; wound healing; coagulation; KW

KW angiogenesis; solid tumour; infection; leukemia; growth factor activity;
 KW cell mediated autoimmune disease; psoriasis; allergy; attherosclerosis

KW T-cell mediated autoimmune disease; psoriasis; allergy; atherogenesis;
KW aneurysms; malignancy; inflammation; histamine; IgE; silicosis; shock;

KW anaphylaxis; malignancy; inflammation; histamine; IgE; silicosis; shock; immunoglobulin E-mediated allergic reaction: rheumatoid arthritis.

KW immunoglobulin E-mediated allergic reaction; rheumatoid arthritis;
KW prostaglandin-independent fever; bone marrow failure; sarcoidosis;

KW
hyper-eqs inop
prostaglandin

XX
 КМ
 1987 г. 10.01.1987 г.

OS Homo sapiens.

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Key

FT	FT	CDS
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PD 12-APR-2001.
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DE 20-NOV-2000.

PF 29-NOV-2000;
YY

06-TTN-1995.

PR 06-JUN-1995;
PR 18-NOV-1998:

FR	10 NOV 1990,
PR	25-JUN-1999:

XX
NOV 67

PA (LIYY/) LI Y.

PA (RUBE/) RUBEN/

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PI Li Y, Ruben

CC (i) a fully defined 329 amino acid sequence (II) fully disclosed in the
 CC specification; and (ii) a polypeptide encoded by the cDNA contained in a
 CC plasmid, and fragments, analogs and derivatives of the polypeptide. The
 CC products of the invention have antiinflammatory, immunomodulatory,
 CC antiparasitic, antiallergic, immunosuppressive, vulnerary, cytostatic,
 CC antiparasitic, antiparasitic, antirheumatic, antithrombotic and vasotropic
 CC activity and can be used for gene therapy. The G-protein chemokine
 CC receptors, HDNR10, (I) are useful for screening for compounds which
 CC activate or inhibit activation of (I). The products of the invention can
 CC also be used for stimulating haematopoiesis, wound healing, coagulation,
 CC angiogenesis, treating solid tumours, chronic infections, leukemia,
 CC T-cell mediated autoimmune diseases, parasitic infections, psoriasis, and
 CC stimulating growth factor activity. HDNR10 is useful for treating
 CC allergy, atherosclerosis, anaphylaxis, malignancy, chronic and acute
 CC inflammation, histamine and immunoglobulin E (IgE)-mediated allergic
 CC reactions, prostaglandin-independent fever, bone marrow failure,
 CC silicosis, sarcoidosis, rheumatoid arthritis, shock and
 CC hyper-eosinophilic syndrome.
 XX
 SQ Sequence 1414 BP; 353 A; 342 C; 312 G; 407 T; 0 other;

Query Match 89.7%; Score 1293.4; DB 22; Length 1414;
 Best Local Similarity 96.6%; Pred. No. 0;
 Matches 1345; Conservative 0; Mismatches 16; Indels 32; Gaps 1;

QY 2 AATTCGCCCAACAGAGCCAGCTCTCCATCTAGTGGACAGGAGAGCTAGCAGCAACCTT 61
 DB 21 ATTCGCCCAACAGAGCCAGCTCTCCATCTAGTGGACAGGAGAGCTAGCAGCAACCTT 80
 QY 62 CCCTTCACTACAAATCTTCAATGCTTGGCCAAAAGAGAGTTAATTCATGTAGACATCT 121
 DB 81 CCCTTCACTACAAATCTTCAATGCTTGGCCAAAAGAGAGTTAATTCATGTAGACATCT 140
 QY 122 ATGTAGCAATTAACCACTATGATGATTAACAGCTTTGCATTCATGGAGGCACTA 181
 DB 141 ATGTAGCAATTAACCACTATGATGATTAACAGCTTTGCATTCATGGAGGCACTA 200
 QY 182 AATACATCTTAGGACTTTATAAAGATCACTTTTATTTATGACAGGAGTGAACAAGAT 241
 DB 201 AATACATCTTAGGACTTTATAAAGATCACTTTTATTTATGACAGGAGTGAACAAGAT 260
 QY 242 GGATTAATCAAGTGTCAAGTCCATCTATGACATCAATTTATATACATGGAGCCCTGCCA 301
 DB 261 GGATTAATCAAGTGTCAAGTCCATCTATGACATCAATTTATATACATGGAGCCCTGCCA 320
 QY 302 AAAATCAATGTGAAGAAATCGAGCCGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 361
 DB 321 AAAATCAATGTGAAGAAATCGAGCCGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 380
 QY 362 CATCTTTGTTGTTGGGCAACATGCTGGTCACTCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 421
 DB 381 CATCTTTGTTGTTGGGCAACATGCTGGTCACTCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 440
 QY 422 GAAGAGCATGACTGACATCTACCTGCTCAACCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 481
 DB 441 GAAGAGCATGACTGACATCTACCTGCTCAACCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 500
 QY 482 TACTGTCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 541
 DB 501 TACTGTCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 560
 QY 542 TCAACTCTTGACAGGCTCTATTTTATPAGGCTTCTCTGGAATCTTCTTCATCATCCT 601
 DB 561 TCAACTCTTGACAGGCTCTATTTTATPAGGCTTCTCTGGAATCTTCTTCATCATCCT 620
 QY 602 CTTGACATCGATAGTACCTGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 661
 DB 621 CTTGACATCGATAGTACCTGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 680
 QY 662 GGTACACCTTTGGGGTGGTGACAAAGTGTGATCACTTGGGTTGGGCTGCTGCTGCTGCT 721
 DB 681 GGTACACCTTTGGGGTGGTGACAAAGTGTGATCACTTGGGTTGGGCTGCTGCTGCTGCT 740

QY 722 CCCAGGAATCATCTTTACAGATCTCAAAAGAGGCTCTTATTACACCTGCAGCTTCA 781
 DB 741 CCCAGGAATCATCTTTACAGATCTCAAAAGAGGCTCTTATTACACCTGCAGCTTCA 800
 QY 782 TTTTCCAT-----ACATTAAGATAGTCACTT 809
 DB 801 TTTTCCATACAGTCAGTATCAATTCGGAAGAAATTTCCAGACATTAAGATAGTCACTT 860
 QY 810 GGGGCTGGCTCTGCGCTGCTGTGTCATGGTCACTGCTGCTGCTGCTGCTGCTGCTGCTGCT 869
 DB 861 GGGGCTGGCTCTGCGCTGCTGTGTCATGGTCACTGCTGCTGCTGCTGCTGCTGCTGCTGCT 920
 QY 870 GCTTCGGTGTGAAAATGAGAAAGAGGACAGGGCTGTGAGGCTTATCTTCAACATCAT 929
 DB 921 GCTTCGGTGTGAAAATGAGAAAGAGGACAGGGCTGTGAGGCTTATCTTCAACATCAT 980
 QY 930 GATTGTTTATTTTCTCTTCTGGGCTCCCTAACAAATTTGCTTCTGCTGCTGCTGCTGCTGCT 989
 DB 981 GATTGTTTATTTTCTCTTCTGGGCTCCCTAACAAATTTGCTTCTGCTGCTGCTGCTGCTGCT 1040
 QY 990 GGAATTTCTTTGGCTCAATTAATTTGAGTACCTTCAACAGGTTGGACCAAGCTATGAGGT 1049
 DB 1041 GGAATTTCTTTGGCTCAATTAATTTGAGTACCTTCAACAGGTTGGACCAAGCTATGAGGT 1100
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 QY 1170 CAAATGCTGTTCTATTTTCCAGAGAGGCTCCCGAGGAGCAAGCTCACTGTTTACACCG 1229
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 QY 1350 GGAGGCTCTTTT 1362
 DB 1401 GGAGGCTCTTT 1413

Search completed: June 8, 2003, 07:47:35
 Job time : 363 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: June 8, 2003, 07:28:02 ; Search time 77 seconds
(without alignments)
5743.219 Million cell updates/sec

Title: US-09-938-703-3

Perfect score: 1442

Sequence: 1 GAATTCCTCCAGAGCCGCA.....AGTATTAGATCCGATTC 1442

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 441362 seqs, 153338381 residues

Total number of hits satisfying chosen parameters: 882724

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

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6: /cgn2_6/ptodata/1/ina/backfiles1.seq: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1442	100.0	1442	4	US-08-833-752-3
2	1382.8	95.9	1477	4	US-08-833-752-2
3	1344	93.2	1344	3	US-09-087-232A-16
4	1302	90.3	1376	3	US-09-087-232A-12
5	1288.6	89.4	1414	3	US-08-466-343D-1
6	1149	79.7	3383	4	US-08-861-105-13
7	1149	79.7	3383	4	US-08-575-967A-1
8	985	68.3	1059	4	US-08-724-984A-3
9	983.4	68.2	1071	3	US-09-087-232A-14
10	982.8	68.2	1071	3	US-09-293-170-3
11	954.6	66.2	1059	4	US-09-517-605-8
12	792	54.9	792	4	US-08-833-752-1
13	727.4	50.4	2440	4	US-08-724-984A-1
14	683.4	47.4	1979	1	US-08-450-393A-3
15	683.4	47.4	1979	5	US-08-446-669-3
16	683.4	47.4	1979	5	PCT-US95-00476-3
17	612.6	42.5	2232	1	US-08-450-393A-1
18	612.6	42.5	2232	3	US-08-446-669-1
19	612.6	42.5	2232	3	PCT-US95-00476-1
20	385.4	26.7	461	3	US-09-087-232A-11
21	330.2	22.9	2156	1	US-08-012-988A-1
22	319.4	22.1	1915	4	US-08-575-967A-3
23	318.2	22.1	1065	4	US-08-847-296B-2
24	294.8	20.4	1607	3	US-08-875-573-19
25	294.8	20.4	1695	4	US-09-232-878-1
26	242	16.8	2961	4	US-09-177-437-1
27	229.8	15.9	1586	1	US-08-461-244-1

28	194.6	13.5	1161	1	US-08-153-848-31	Sequence 31, Appl
29	194.6	13.5	1161	5	PCT-US93-11153-31	Sequence 31, Appl
30	194.6	13.5	2254	1	US-08-153-848-27	Sequence 27, Appl
31	194.6	13.5	2254	3	US-09-299-843A-27	Sequence 27, Appl
32	194.6	13.5	2254	4	US-09-088-337B-27	Sequence 27, Appl
33	194.6	13.5	2254	5	PCT-US93-11153-27	Sequence 27, Appl
34	194.6	13.5	3119	3	US-09-299-843A-31	Sequence 31, Appl
35	194.6	13.5	3119	4	US-09-088-337B-31	Sequence 31, Appl
36	184.2	12.8	1050	4	US-08-681-192-1	Sequence 1, Appl
37	165	11.4	239	4	US-09-481-288-1	Sequence 1, Appl
38	150.6	10.4	1137	4	US-09-045-583-6	Sequence 6, Appl
39	150.6	10.4	1137	4	US-09-534-185-6	Sequence 6, Appl
40	150.6	10.4	1664	4	US-09-045-583-4	Sequence 4, Appl
41	150.6	10.4	1664	4	US-09-534-185-4	Sequence 4, Appl
42	142.8	9.9	2751	1	US-08-153-848-23	Sequence 23, Appl
43	142.8	9.9	2751	3	US-09-299-843A-23	Sequence 23, Appl
44	142.8	9.9	2751	4	US-09-088-337B-23	Sequence 23, Appl
45	142.8	9.9	2751	5	PCT-US93-11153-23	Sequence 23, Appl

ALIGNMENTS

RESULT 1
US-08-833-752-3
; Sequence 3, Application US/08833752
; Patent No. 6448375
; GENERAL INFORMATION:
; APPLICANT: SAMSON, MICHEL
; APPLICANT: PARMENTIER, MARC
; APPLICANT: VASSART, GILBERT
; APPLICANT: LIBERT, FREDERICK
; TITLE OF INVENTION: ACTIVE AND INACTIVE CC-CHEMOKINES RECEPTOR
; TITLE OF INVENTION: AND NUCLEIC ACID MOLECULES ENCODING SAID RECEPTOR
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Knobe, Martens, Olson & Bear
; STREET: 620 Newport Center Drive 16th Floor
; CITY: Newport Beach
; STATE: CA
; COUNTRY: U.S.A.
; ZIP: 92660
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/833,752
; FILING DATE: 9-APR-1997
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Altman, Daniel E
; REGISTRATION NUMBER: 34,115
; REFERENCE/DOCKET NUMBER:
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1442 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 240..884
; US-08-833-752-3

Query Match 100.0%; Score 1442; DB 4; Length 1442;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 1442; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GAATTCCTCCAGAGCCGATCTCCATCTAGTGGACAGGAGTAGCGCAACT 60
|||||

Db 1 GAATCCCAACAGAGCAAGCTCTCCATCTAGTGCAGAGGAAAGCTAGACCAAACT 60
QY TCCCTTCACTACAAACTTCATTGCTGGCCAAAAGAGAGTAAATTCATGTAGACATC 120
Db 61 TCCCTTCACTACAAACTTCATTGCTGGCCAAAAGAGAGTAAATTCATGTAGACATC 120
QY TATGTAGGCAATTAAGCACTATGTAGATATAAACAAGTTGCAATCATGAGGGCAACT 180
Db 121 TATGTAGGCAATTAAGCACTATGTAGATATAAACAAGTTGCAATCATGAGGGCAACT 180
QY AAATACATCTAGGACTTTATAAGATCACTTTTATTATGACAGGGTGAACAAGA 240
Db 181 AAATACATCTAGGACTTTATAAGATCACTTTTATTATGACAGGGTGAACAAGA 240
QY TGGATATCAAGTGTCAAGTCCAATCTATGACATCAATTAATATACATCGGAGCCCTGCC 300
Db 241 TGGATATCAAGTGTCAAGTCCAATCTATGACATCAATTAATATACATCGGAGCCCTGCC 300
QY AAAAATCAATGTGAAGCAATCGAGCCGCCCTCTGCTCTACTACTACTACTACTACT 360
Db 301 AAAAATCAATGTGAAGCAATCGAGCCGCCCTCTGCTCTACTACTACTACTACTACT 360
QY TCACTTTGGTTTTGTGGCAACATGCTGGTCACTCTCTCATCTCTGATAAAGTCAAAAGGC 420
Db 361 TCACTTTGGTTTTGTGGCAACATGCTGGTCACTCTCTCATCTCTGATAAAGTCAAAAGGC 420
QY TGAAGAGATGACTGACATCTACCTGCTCAACCTGGCCATCTGACCTGTTTTCCTTC 480
Db 421 TGAAGAGATGACTGACATCTACCTGCTCAACCTGGCCATCTGACCTGTTTTCCTTC 480
QY TTAAGTCCCTTCTGGGCTCACTATGCTGGCCGCAAGTGGGACTTGGAAATACAACTG 540
Db 481 TTAAGTCCCTTCTGGGCTCACTATGCTGGCCGCAAGTGGGACTTGGAAATACAACTG 540
QY GTCAACTCTTGACAGGCTCTATTTATAGGCTTCTCTGGAATCTTCTCATCATCC 600
Db 541 GTCAACTCTTGACAGGCTCTATTTATAGGCTTCTCTGGAATCTTCTCATCATCC 600
QY TCCGTACATCATAGTACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 660
Db 601 TCCGTACATCATAGTACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 660
QY CGGTACCTTTGGGCTGTGACAAAGTGTGATCACTTGGGTGGTGTGCTGCTGCTGCTC 720
Db 661 CGGTACCTTTGGGCTGTGACAAAGTGTGATCACTTGGGTGGTGTGCTGCTGCTGCTC 720
QY TCCAGATATCATCTTACAGATCTCAAAAGAGTCTTCAATACACCTGACGCTGCTC 780
Db 721 TCCAGATATCATCTTACAGATCTCAAAAGAGTCTTCAATACACCTGACGCTGCTC 780
QY ATTTTGCATACATTAAGATAGTCACTTTGGGCTGCTGCTGCTGCTGCTGCTGCTGCTC 840
Db 781 ATTTTGCATACATTAAGATAGTCACTTTGGGCTGCTGCTGCTGCTGCTGCTGCTGCTC 840
QY ATCTGTACTCGGGAATCCFAAAAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTC 900
Db 841 ATCTGTACTCGGGAATCCFAAAAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTC 900
QY AGGCTGTGAGGCTTATCTTACCATCATGATTTGTTTATTTCTTCTTCTGCTGCTGCTC 960
Db 901 AGGCTGTGAGGCTTATCTTACCATCATGATTTGTTTATTTCTTCTTCTGCTGCTGCTC 960
QY AACATGCTCTCTCTGCAACACTTCCAGGAATCTTTTGGGCTGCTGCTGCTGCTGCTGCTC 1020
Db 961 AACATGCTCTCTCTGCAACACTTCCAGGAATCTTTTGGGCTGCTGCTGCTGCTGCTGCTC 1020
QY TCTAACAGTGTGACCAAGCTATGCAAGTGTGACAGACTCTTGGGATGACGACTGCTGCTC 1080
Db 1021 TCTAACAGTGTGACCAAGCTATGCAAGTGTGACAGACTCTTGGGATGACGACTGCTGCTC 1080
QY ATCAACCCCATCATCTATGCTTGTGCGGGAGAGTTTCAAGAACTTCTTGTAGCTTC 1140
Db 1081 ATCAACCCCATCATCTATGCTTGTGCGGGAGAGTTTCAAGAACTTCTTGTAGCTTC 1140

QY 1141 TTCCAAAGCACATTCGCAACGCTTCTCAATCTGTTCTTATTTCCAGCAAGGCT 1200
Db 1141 TTCCAAAGCACATTCGCAACGCTTCTCAATCTGTTCTTATTTCCAGCAAGGCT 1200
QY CCGAGGAGCAAGCTCAGTTTACCCGATCCACTGGGAGCAGGAATATCTGTGGC 1260
Db 1201 CCGAGGAGCAAGCTCAGTTTACCCGATCCACTGGGAGCAGGAATATCTGTGGC 1260
QY TTGTGACACGACTCAAGTGGCTGGTGGCCAGTCCAGTCTGTCACATGCTGCTT 1320
Db 1261 TTGTGACACGACTCAAGTGGCTGGTGGCCAGTCCAGTCTGTCACATGCTGCTT 1320
QY TCATACACAGCTTGGGCTGGGCTGGGCTGGGCTGGGCTGGGCTGGGCTGGGCTGGG 1380
Db 1321 TCATACACAGCTTGGGCTGGGCTGGGCTGGGCTGGGCTGGGCTGGGCTGGGCTGGG 1380
QY TAGAGGCTCTAAGATTCATTCATTTTGGCATCTGTTTAAAGTAGATAGATCCGAAT 1440
Db 1381 TAGAGGCTCTAAGATTCATTCATTTTGGCATCTGTTTAAAGTAGATAGATCCGAAT 1440
QY 1441 TC 1442
Db 1441 TC 1442

RESULT 2
US-08-833-752-2
; Sequence 2, Application US/08833752
; Patent No. 6448375
; GENERAL INFORMATION:
; APPLICANT: SAMSON, MICHEL
; APPLICANT: PARMENTIER, MARC
; APPLICANT: VASSART, GILBERT
; APPLICANT: LIBERT, FREDERICK
; TITLE OF INVENTION: ACTIVE AND INACTIVE CC-CHEMOKINES RECEPTOR
; TITLE OF INVENTION: AND NUCLEIC ACID MOLECULES ENCODING SAID RECEPTOR
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Knobbe, Martens, Olson & Bear
; STREET: 620 Newport Center Drive 16th Floor
; CITY: Newport Beach
; STATE: CA
; COUNTRY: U.S.A.
; ZIP: 92660
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/833,752
; FILING DATE: 9-APR-1997
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Altman, Daniel E
; REGISTRATION NUMBER: 34,115
; REFERENCE/DOCKET NUMBER:
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1477 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 240..1295
US-08-833-752-2

Query Match 95.9%; Score 1382.8; DB 4; Length 1477;
Best Local Similarity 97.4%; Pred. No. 0;
Matches 1439; Conservative 0; Mismatches 3; Indels 35; Gaps 2;

LOCATION: 240..887

US-09-087-232A-16

Query Match 93.2%; Score 1344; DB 3; Length 1344;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 1344; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAATTCCTCCACAGAGCCAGCTCCATCTAGTGGACAGGAGGAGCTAGCAGCAACCT 60
 DB 1 GAATTCCTCCACAGAGCCAGCTCCATCTAGTGGACAGGAGGAGCTAGCAGCAACCT 60
 QY 61 TCCCTTCACTACAAAATTCATCTGCTGGCCAAAAGAGAGTTAAATCAATAGACATC 120
 DB 61 TCCCTTCACTACAAAATTCATCTGCTGGCCAAAAGAGAGTTAAATCAATAGACATC 120
 QY 121 TATGTAGCAATTAAGCAATTAATGATGATATAAAGAGTTGCAATCGAGGCAACT 180
 DB 121 TATGTAGCAATTAAGCAATTAATGATGATATAAAGAGTTGCAATCGAGGCAACT 180
 QY 181 AAATACATCTAGGACCTTATAAAGATCACTTTTATTTATGACAGAGGTGGAACAGA 240
 DB 181 AAATACATCTAGGACCTTATAAAGATCACTTTTATTTATGACAGAGGTGGAACAGA 240
 QY 241 TGGATTATCAAGTGTCAAGTCCATCTATGACATCAATTAATATACATCGGAGCCCTGCC 300
 DB 241 TGGATTATCAAGTGTCAAGTCCATCTATGACATCAATTAATATACATCGGAGCCCTGCC 300
 QY 301 AAAAATCAATGTGAAGCAAAATCCGAGCCCGCTCTGCTCCGCTCTACTCAGTGGGT 360
 DB 301 AAAAATCAATGTGAAGCAAAATCCGAGCCCGCTCTGCTCCGCTCTACTCAGTGGGT 360
 QY 361 TCATCTTTGGTTTGTGGCAACATGCTGCTCATCTCATCTGATAAACTGCAAAAGGC 420
 DB 361 TCATCTTTGGTTTGTGGCAACATGCTGCTCATCTCATCTGATAAACTGCAAAAGGC 420
 QY 421 TGAAGACATGACTGACATFACCTGCTCAACCTGGCCATCTGACCTGTTTTCCCTTC 480
 DB 421 TGAAGACATGACTGACATFACCTGCTCAACCTGGCCATCTGACCTGTTTTCCCTTC 480
 QY 481 TTACTGTCCTCTCTGGGCTCACTATGCTGCGCCCATCGGACTTGGAAATACAATGT 540
 DB 481 TTACTGTCCTCTCTGGGCTCACTATGCTGCGCCCATCGGACTTGGAAATACAATGT 540
 QY 541 GTCAACTCTTGACAGGCTCTATTTATAGGCTTCTCTGGAATCTTCTTCATCATCC 600
 DB 541 GTCAACTCTTGACAGGCTCTATTTATAGGCTTCTCTGGAATCTTCTTCATCATCC 600
 QY 601 TCTTGACAAATGATAGTACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 660
 DB 601 TCTTGACAAATGATAGTACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 660
 QY 661 CGGTCACTTTGGGTTGGTGAAGTGTGATCACTTGGGTTGGTGGTGGTGGTGGTGGT 720
 DB 661 CGGTCACTTTGGGTTGGTGAAGTGTGATCACTTGGGTTGGTGGTGGTGGTGGTGGT 720
 QY 721 TCCAGGAATCATCTTTACAGATCTCAAAAAGAGGCTTCAATACACTGCAGCTCTC 780
 DB 721 TCCAGGAATCATCTTTACAGATCTCAAAAAGAGGCTTCAATACACTGCAGCTCTC 780
 QY 781 ATTTTCCATCATTAAGTGTGATCACTTGGGCTGGTGGTGGTGGTGGTGGTGGTGGT 840
 DB 781 ATTTTCCATCATTAAGTGTGATCACTTGGGCTGGTGGTGGTGGTGGTGGTGGTGGT 840
 QY 841 ATCTGCTACTCGGGAATCTTAAAACTCTGCTTGGTGTGGAATGAGAGAGGAGGAC 900
 DB 841 ATCTGCTACTCGGGAATCTTAAAACTCTGCTTGGTGTGGAATGAGAGAGGAGGAC 900
 QY 901 AGGCTGTAGGCTTATCTTCAACATCATGATGTTATTTCTCTCTGGGCTCCCTTAC 960
 DB 901 AGGCTGTAGGCTTATCTTCAACATCATGATGTTATTTCTCTCTGGGCTCCCTTAC 960
 QY 961 ACATGTCCTCTCTGACACCTTCCAGAACTTCTTGGCTGAATTAATTCAGTAGC 1020

DB 961 AACATTGCTCTCTCTGACACACTTCCAGGAATCTTTGGCTGGAATAATTCAGTAGC 1020
 QY 1021 TCTAACAGGTTGGACCAAGCTATGAGGTGACAGACACTCTTTGGGATGACGCACTGCTGC 1080
 DB 1021 TCTAACAGGTTGGACCAAGCTATGAGGTGACAGACACTCTTTGGGATGACGCACTGCTGC 1080
 QY 1081 ATCAACCCCATCATCTATGCTTTGTCGGGGAAGATTGAGAACTACCTCTTAGTCTTC 1140
 DB 1081 ATCAACCCCATCATCTATGCTTTGTCGGGGAAGATTGAGAACTACCTCTTAGTCTTC 1140
 QY 1141 TTCCAAAGACACATGTCGCAACGCTTCTGCAATGCTGTTCTATTTTCCAGCAAGAGCT 1200
 DB 1141 TTCCAAAGACACATGTCGCAACGCTTCTGCAATGCTGTTCTATTTTCCAGCAAGAGCT 1200
 QY 1201 CCGAGGAGCAAGCTCAGTTTACACCCGATCCACTGGGGAGCAGGAATATCTGTGGGC 1260
 DB 1201 CCGAGGAGCAAGCTCAGTTTACACCCGATCCACTGGGGAGCAGGAATATCTGTGGGC 1260
 QY 1261 TTGTGACAGGACTCAAGTGGGCTGGTCCAGCTGAGAGTTGTGCATGGCTTAGTTT 1320
 DB 1261 TTGTGACAGGACTCAAGTGGGCTGGTCCAGCTGAGAGTTGTGCATGGCTTAGTTT 1320
 QY 1321 TCATACACAGCTGGGCTGGGCT 1344
 DB 1321 TCATACACAGCTGGGCTGGGCT 1344

RESULT 4

US-09-087-232A-12
 ; Sequence 12, Application US/09087232A
 ; Patent No. 6153431
 ; GENERAL INFORMATION:
 ; APPLICANT: Quillent et al.
 ; TITLE OF INVENTION: HUMAN IMMUNODEFICIENCY VIRUS CO-RECEPTOR
 ; NUMBER OF SEQUENCES: 23
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Baker & Botts, L.L.P. attn. Lisa Kole
 ; CITY: New York
 ; STATE: New York
 ; COUNTRY: USA
 ; ZIP: 10112
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; OPERATING SYSTEM: IBM PC compatible
 ; SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/09/087,232A
 ; FILING DATE: 28 MAY 1998
 ; CLASSIFICATION: 435
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 60/048,057
 ; FILING DATE: 30 MAY 1997
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: KOLE, LISA B.
 ; REGISTRATION NUMBER: 35,225
 ; REFERENCE/DOCKET NUMBER: AP 31115
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (212) 408-2628
 ; TELEFAX: (212) 765-2519
 ; INFORMATION FOR SEQ ID NO: 12:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 1376 base pairs
 ; TYPE: nucleic acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: DNA (genomic)
 ; FEATURE:
 ; NAME/KEY: CDS
 ; LOCATION: 240..1298
 ; US-09-087-232A-12

Query Match 90.38; Score 1302; DB 3; Length 1376;
Best Local Similarity 97.74; Pred. No. 0;
Matches 1344; Conservative 0; Mismatches 0; Indels 32; Gaps 1;

QY 1 GAATTCCTCCCAACAGAGCCAAAGCTCCATCTAGTGGACAGGAAGCTAGCAGCAAACT 60
DB 1 GAATTCCTCCCAACAGAGCCAAAGCTCCATCTAGTGGACAGGAAGCTAGCAGCAAACT 60

QY 61 TCCTTCTACTACAAAACCTTCAATGCTTGGCCAAAAGAGAGGTTAATCAATGAGACATC 120
DB 61 TCCTTCTACTACAAAACCTTCAATGCTTGGCCAAAAGAGAGGTTAATCAATGAGACATC 120

QY 121 TAGTAGGCAATTAATAACCTTATGATGATATAAAGCAGTTCATGAGGAGCACT 180
DB 121 TAGTAGGCAATTAATAACCTTATGATGATATAAAGCAGTTCATGAGGAGCACT 180

QY 181 AATACATCTAGGACCTTATAAAGATCACTTTTATTAATGACAGAGGTTGAACAAGA 240
DB 181 AATACATCTAGGACCTTATAAAGATCACTTTTATTAATGACAGAGGTTGAACAAGA 240

QY 241 TGGATTATCAAGTCTCAAGTCCAAATGATGACATCAATTTATTAATGACATCGGAGCCCTGCC 300
DB 241 TGGATTATCAAGTCTCAAGTCCAAATGATGACATCAATTTATTAATGACATCGGAGCCCTGCC 300

QY 301 AAAAAATCAATGTGAAGCAAAATCGCAGCCGCTCTGCTCGCTCTACTCACTGGTGT 360
DB 301 AAAAAATCAATGTGAAGCAAAATCGCAGCCGCTCTGCTCGCTCTACTCACTGGTGT 360

QY 361 TCATCTTTGGTTTTGGGCAACATGCTGTCTATCTCTATCTCTATCTGATAAAGC 420
DB 361 TCATCTTTGGTTTTGGGCAACATGCTGTCTATCTCTATCTCTATCTGATAAAGC 420

QY 421 TGAAGCATGACATGACATCTACCTGCTCAACCTGCGCACTCTGACCTGTTTTGCTTC 480
DB 421 TGAAGCATGACATGACATCTACCTGCTCAACCTGCGCACTCTGACCTGTTTTGCTTC 480

QY 481 TTACTGTCCTCTCTGGGCTCACTATGCTGCGCCAGTGGGACTTTGGAAATACAAATG 540
DB 481 TTACTGTCCTCTCTGGGCTCACTATGCTGCGCCAGTGGGACTTTGGAAATACAAATG 540

QY 541 GTCAACTCTTGACAGGCTCTATTTATPAGGCTTCTCTGGAATCTTCTCATCATCC 600
DB 541 GTCAACTCTTGACAGGCTCTATTTATPAGGCTTCTCTGGAATCTTCTCATCATCC 600

QY 601 TCGTCACAAATGATAGTACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 660
DB 601 TCGTCACAAATGATAGTACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 660

QY 661 CGGTCACTTTGGGGTGGTGACAAGTGTGATCACTTGGGTGGTGGTGGTGGTGGTGGT 720
DB 661 CGGTCACTTTGGGGTGGTGACAAGTGTGATCACTTGGGTGGTGGTGGTGGTGGTGGT 720

QY 721 TCCAGGAATCATCTTACAGATCTCAAAAGAGGCTTCAATTAACCTGACGCTC 780
DB 721 TCCAGGAATCATCTTACAGATCTCAAAAGAGGCTTCAATTAACCTGACGCTC 780

QY 781 ATTTTCCAT-----ACATTAAGATAGTACT 808
DB 781 ATTTTCCATAGCAGTCAATTAATTCGGAAGAAATTCAGACATTAAGATAGTACT 840

QY 809 TGGGGTGGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 868
DB 809 TGGGGTGGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 868

QY 869 TGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 928
DB 869 TGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 928

QY 929 TGAATTTTATTTCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 988
DB 929 TGAATTTTATTTCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 988

QY 961 TGATTTGTTATTTCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1020
DB 961 TGATTTGTTATTTCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1020

QY 989 AGGAATCTTTGGCTGAATAATTCAGTAGTCTTAACAGAGTTGGACCAAGCTATGCAGG 1048
DB 1021 AGGAATCTTTGGCTGAATAATTCAGTAGTCTTAACAGAGTTGGACCAAGCTATGCAGG 1080

QY 1049 TGACAGAGACTCTTGGGATGACGCACTGCTGATCAACCCCAATCATCTATGCTTTGTGG 1108
DB 1081 TGACAGAGACTCTTGGGATGACGCACTGCTGATCAACCCCAATCATCTATGCTTTGTGG 1140

QY 1109 GGGAGAGTTCAAGAACTTCTTATTTCCAGCAAGAGGCTCCCGAGGAGCAAGCTCAGTTTACACC 1168
DB 1141 GGGAGAGTTCAAGAACTTCTTATTTCCAGCAAGAGGCTCCCGAGGAGCAATTTGCCAAGCTTCT 1200

QY 1169 GCAAAAGCTGTTCTTATTTCCAGCAAGAGGCTCCCGAGGAGCAAGCTCAGTTTACACC 1228
DB 1201 GCAAAAGCTGTTCTTATTTCCAGCAAGAGGCTCCCGAGGAGCAAGCTCAGTTTACACC 1260

QY 1229 GATCCACTGGGAGGAGCAATATCTGTGGCTTGTGACACGAGCTCAAGTGGGCTGGTG 1288
DB 1261 GATCCACTGGGAGGAGCAATATCTGTGGCTTGTGACACGAGCTCAAGTGGGCTGGTG 1320

QY 1289 ACCCAGTCAGAGTTGTGCACATGCTTAGTTTATACACAGCTGGGCTGGGGGT 1344
DB 1321 ACCCAGTCAGAGTTGTGCACATGCTTAGTTTATACACAGCTGGGCTGGGGGT 1376

RESULT 5
US-08-466-343D-1
; Sequence 1, Application US/08466343D
; Patent No. 6025154
; GENERAL INFORMATION:
; APPLICANT: LI, YI
; TITLE OF INVENTION: POLYNUCLEOTIDES ENCODING HUMAN G-PROTEIN
; TITLE OF INVENTION: CHEMOKINE RECEPTOR HDNR10 (AS AMENDED)
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.
; STREET: 1100 NEW YORK AVE., NW, SUITE 600
; CITY: WASHINGTON
; STATE: DC
; COUNTRY: USA
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/466,343D
; FILING DATE: 06-JUN-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: STEFFE, ERIC K.
; REGISTRATION NUMBER: 36,688
; REFERENCE/DOCKET NUMBER: 1488.1150000/EKS/KLM
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 371-2600
; TELEFAX: (202) 371-2540
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1414 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 259..1314
US-08-466-343D-1

Query Match 89.44; Score 1288.6; DB 3; Length 1414;
Best Local Similarity 96.34; Pred. No. 0;
Matches 1342; Conservative 0; Mismatches 19; Indels 32; Gaps 1;

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Db      1101  GACAGAGACTCTTGGGATGAGCCACTGCTGCATCAACCCCATCATCTATGCTTTGTGCG 1160
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QY      1110  GGAGAAGTTTCAGAAACTACCTCTTTAGTCTTCTTCCAAAGACACATGGCAAAGCTTTCTG 1169
|||||
Db      1161  GGAGAAGTTTCAGAAACTACCTCTTTAGTCTTCTTCCAAAGACACATGGCAAAGCTTTCTG 1220
|||||
QY      1170  CAAATGCTGTCTATTCTTCCAGCAGAGGCTCCGAGCGAGCAAGCTCAGTTTACACCG 1229
|||||
Db      1221  CAAATGCTGTCTATTCTTCCAGCAGAGGCTCCGAGCGAGCAAGCTCAGTTTACACCG 1280
|||||
QY      1230  ATCCACTGGGAGCAGGAAATATCTGTGGGCTTGTCACGGACTCAAGTGGCTGGTGA 1289
|||||
Db      1281  ATCCACTGGGAGCAGGAAATATCTGTGGGCTTGTCACGGACTCAAGTGGCTGGTGA 1340
|||||
QY      1290  CCAGTTCAGAGTTGTCACATGGCTTAGTTTTCATACACAGCCTGGGCTGGGGGTGGT 1349
|||||
Db      1341  CCAGTTCAGAGTTGTCACATGGCTTAGTTTTCATACACAGCCTGGGCTGGGGGTGGG 1400
|||||
QY      1350  GGAGGCTCTTTT 1362
|||||
Db      1401  GGAAGAGCTTT 1413
|||||

RESULT 6
US-08-861-105-13
: Sequence 13, Application US/08861105
: Patent No. 6258527
: GENERAL INFORMATION:
: APPLICANT: LITTMAN, DAN R.
: APPLICANT: DENG, HONGKUI
: APPLICANT: ELMIEIER, WILFRIED
: APPLICANT: LANDAU, NATHANIEL R.
: APPLICANT: LIU, RONG
: TITLE OF INVENTION: G-COUPLED RECEPTORS ASSOCIATED WITH
: TITLE OF INVENTION: MACROPHAGE-TROPIC HIV, AND DIAGNOSTIC AND THERAPEUTIC
: TITLE OF INVENTION: USES THEREOF
: NUMBER OF SEQUENCES: 14
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: David A. Jackson, Esq.
: STREET: 411 Hackensack Ave, Continental Plaza, 4th
: STREET: Floor
: CITY: Hackensack
: STATE: New Jersey
: COUNTRY: USA
: ZIP: 07601
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: PatentIn Release #1.0, Version #1.30
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/861,105
: FILING DATE:
: CLASSIFICATION: 436
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 08/666,020
: FILING DATE: 19-JUN-1996
: CLASSIFICATION: 436
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 08/227,319
: FILING DATE: 13-APR-1994
: ATTORNEY/AGENT INFORMATION:
: NAME: Jackson Esq., David A.
: REGISTRATION NUMBER: 26,742
: REFERENCE/DOCKET NUMBER: 1049-1-004 N1
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 201-487-5800
: TELEFAX: 201-343-1684
: INFORMATION FOR SEQ ID NO: 13:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 3383 base pairs
: TYPE: nucleic acid

```


STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: CDNA
HYPOTHETICAL: NO
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
US-08-861-105-13

Query Match 79.7%; Score 1149; DB 4; Length 3383;
Best Local Similarity 96.8%; Pred. No. 0;
Matches 1207; Conservative 0; Mismatches 5; Indels 35; Gaps 2;

224 CACAGGGTGGACAGAGATGATATCAAGTGTCAAGTCAATCAATCTATGACATCAATATTA 283
Db |
39 CCCGGGTGGACAGAGATGATATCAAGTGTCAAGTGTCAATCTATGACATCAATATTA 98
Db |
284 TACATCGGAGCCCTGCCAAAAATCAATGTGAAGCAAAATCGCAGCCGCCCTCTCGCTCC 343
Qy |
Db |
99 TACATCGGAGCCCTGCCAAAAATCAATGTGAAGCAAAATCGCAGCCGCCCTCTCGCTCC 158
Db |
344 GCTCTACTCACTGTGTTCATCTTTGGTTTGGGCAACATGCTGGTCACTCTCATCT 403
Qy |
Db |
159 GCTCTACTCACTGTGTTCATCTTTGGTTTGGGCAACATGCTGGTCACTCTCATCT 218
Db |
404 GATAAAGTCAAAAGGCTGAAGCAGCATGACATCTACCTGCTCAACCTGGCCATCTC 463
Qy |
Db |
219 GATAAAGTCAAAAGGCTGAAGCAGCATGACATCTACCTGCTCAACCTGGCCATCTC 278
Db |
464 TGACCHGTTTTCTTCTACTGTCCCTTCTGGGCTCACTATGCTGGCCGCCAGTGGGA 523
Qy |
Db |
279 TGACCHGTTTTCTTCTACTGTCCCTTCTGGGCTCACTATGCTGGCCGCCAGTGGGA 338
Db |
524 CTTTGGAAATACAAATGTCTCACTCTTGACAGGGCTCTATTTATAGGCTTCTTCTCGG 583
Qy |
Db |
339 CTTTGGAAATACAAATGTCTCACTCTTGACAGGGCTCTATTTATAGGCTTCTTCTCGG 398
Db |
584 AATCTTCTTCAATCTCTCTGACATCGATAGTACCTGGCTGCTGCCATGCTGTGT 643
Qy |
Db |
399 AATCTTCTTCAATCTCTCTGACATCGATAGTACCTGGCTGCTGCCATGCTGTGT 458
Qy |
Db |
644 TGCTTTAAAGCCAGGAGGCTCACCTTTGGGGTGGTGAAGTGTGATCATCTTGGTGT 703
Qy |
Db |
459 TGCTTTAAAGCCAGGAGGCTCACCTTTGGGGTGGTGAAGTGTGATCATCTTGGTGT 518
Db |
704 GGCTGTGTTTGGCTCTCCAGGAATCATCTTTACAGATCTCAAAAGAGGCTCTCA 763
Qy |
Db |
519 GGCTGTGTTTGGCTCTCCAGGAATCATCTTTACAGATCTCAAAAGAGGCTCTCA 578
Db |
764 TTACACTGCGAGCTCTCATTTTCCAT-----AC 791
Qy |
Db |
579 TTACACTGCGAGCTCTCATTTTCCATATCAGTCAATATCTGGAAGAATTTCCAGAC 638
Qy |
Db |
792 ATTAAGATAGTCAATCTTGGGGTGGTCTCGCTGCTGTCATGTCATCTGTCATCTC 851
Qy |
Db |
639 ATTAAGATAGTCAATCTTGGGGTGGTCTCGCTGCTGTCATGTCATCTGTCATCTC 698
Db |
852 GGAATCTCTAAAGTCTGCTGCTGGTGTGGAATGAGAAGAGGACAGGGCTGTGAG 911
Qy |
Db |
699 GGAATCTCTAAAGTCTGCTGCTGGTGTGGAATGAGAAGAGGACAGGGCTGTGAG 758
Db |
912 GCTTATCTTCAACATCATGATGTTTATTTCTCTGCTGGCTCCCTACAAATGTCCT 971
Qy |
Db |
759 GCTTATCTTCAACATCATGATGTTTATTTCTCTGCTGGCTCCCTACAAATGTCCT 818
Db |
972 TCTCCGTAACACTCTCCAGGAATCTTTGGGCTGAATATGTCAGTACCTTACAGGTT 1031
Qy |
Db |
819 TCTCCGTAACACTCTCCAGGAATCTTTGGGCTGAATATGTCAGTACCTTACAGGTT 878
Db |
1032 GGACCAAGCATATGACAGTCTTGGGATGAGCACTGCTGTCATCAACACCCAT 1091
Qy |
Db |
879 GGACCAAGCATATGACAGTCTTGGGATGAGCACTGCTGTCATCAACACCCAT 938
Db |
1092 CATCTATGCTTTTGGGGGAGAAGTTCAGAAACTACCTCTTAGTCTTCTTCCAAAAGCA 1151
Qy |

939 CATCTATGCTTTGTCGGGGAGAGTTCAGAACTACCTCTTAGTCTTCTTCCAAAAGCA 998
Qy |
1152 CATTGCCAAACGCTTCTGCAATGCTTCTTATTTTCCAGCAAGAGGTCCTCCGAGCAGC 1211
Db |
999 CATTGCCAAACGCTTCTGCAATGCTTCTTATTTTCCAGCAAGAGGTCCTCCGAGCAGC 1058
Db |
1212 AAGCTCAGTTTACACCCGATCCACTGGGAGCAGCAAAATATCTGTGGGCTTGTGACACGG 1271
Qy |
Db |
1059 AAGCTCAGTTTACACCCGATCCACTGGGAGCAGCAAAATATCTGTGGGCTTGTGACACGG 1118
Db |
1272 ACTCAAGTGGGCTGTGACCCAGTGTGTCACATGCTTACTTTTTCATACACAGC 1331
Qy |
Db |
1119 ACTCAAGTGGGCTGTGACCCAGTGTGTCACATGCTTACTTTTTCATACACAGC 1178
Db |
1332 CTGGGCTGGGGTGGG---TTGGGAGGCTTTTAAAAGGAAGTACTTGTATAGAGGT 1388
Qy |
Db |
1179 CTGGGCTGGGGTGGGGTGGGAGAGGCTTTTAAAAGGAAGTACTTGTATAGAGGT 1238
Db |
1389 CTAAGATTCATCAATTTATTTGGCATCTCTTTAAAGTAGATTAGATC 1435
Qy |
Db |
1239 CTAAGATTCATCAATTTATTTGGCATCTCTTTAAAGTAGATTAGATC 1285
Db |

RESULT 7

US-08-575-967A-1
; Sequence 1, Application US/08575967A
; Patent No. 6265184
; GENERAL INFORMATION:
; APPLICANT: Gray et al.
; TITLE OF INVENTION: Chemokine Receptor Materials and Methods
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 6300 Sears Tower, 233 S. Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/575,967A
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: No. 6265184and, Greta E.
; REGISTRATION NUMBER: 35,302
; REFERENCE/DOCKET NUMBER: 32918
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 206-485-1900
; TELEFAX: 206-485-1662
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3383 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: CDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 55..1110
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: /= "88C polynucleotide and amino acid
US-08-575-967A-1

Query Match 79.7%; Score 1149; DB 4; Length 3383;
Best Local Similarity 96.8%; Pred. No. 0;
Matches 1207; Conservative 0; Mismatches 5; Indels 35; Gaps 2;

QY	224	CACAGGTTGGAACAAGATGGATATCAAGTGTCAAGTCCAATCTATGACATCAATATTATTA	283
Db	39	CCCGGGTGGACAAGATGGATATCAAGTGTCAAGTCCAATCTATGACATCAATATTATTA	98
QY	284	TACATCGGAGCCCTGCCAAAAATCAATGTGAACAAATCGAGCCCGCTCTCGCTCC	343
Db	99	TACATCGGAGCCCTGCCAAAAATCAATGTGAACAAATCGAGCCCGCTCTCGCTCC	158
QY	344	GCTCTACTCACTGGTCTTCATCTTTGGTTTTGTGGCAACATGCTGGTCACTCTCATGCT	403
Db	159	GCTCTACTCACTGGTCTTCATCTTTGGTTTTGTGGCAACATGCTGGTCACTCTCATGCT	218
QY	404	GATAAATCGAAAAGCTGAAGAGCAGTACATCTACCTGTGCAACCTGGCCATCTC	463
Db	219	GATAAATCGAAAAGCTGAAGAGCAGTACATCTACCTGTGCAACCTGGCCATCTC	278
QY	464	TGACCTGTTTTTCCCTTCTACTGTGCCCTTCCTGGGCTCAGTATGTCGCCGCCAGTGGGA	523
Db	279	TGACCTGTTTTTCCCTTCTACTGTGCCCTTCCTGGGCTCAGTATGTCGCCGCCAGTGGGA	338
QY	524	CTTTGGAAATACAAATGTGCAACTCTGTGACGGGCTCTATTTATAGGCTTCTTCFCGG	583
Db	339	CTTTGGAAATACAAATGTGCAACTCTGTGACGGGCTCTATTTATAGGCTTCTTCFCGG	398
QY	584	AATCTTCTTCATCATCCCTCGTGAACATCATAGTACTGGCTGCTGCTCATCTGCTGT	643
Db	399	AATCTTCTTCATCATCCCTCGTGAACATCATAGTACTGGCTGCTGCTCATCTGCTGT	458
QY	644	TGCTTTAAAGCCAGACGGTCACTTTGGGTTGGTGACAACTGTGATCACTTTGGTGGT	703
Db	459	TGCTTTAAAGCCAGACGGTCACTTTGGGTTGGTGACAACTGTGATCACTTTGGTGGT	518
QY	704	GGCTGTGTTGGCTCTCTCCAGGAATCATCTTTACCAGATCTCAAAAAGAGGCTTCA	763
Db	519	GGCTGTGTTGGCTCTCTCCAGGAATCATCTTTACCAGATCTCAAAAAGAGGCTTCA	578
QY	764	TTACACCTGGACGCTTCATTTTTCAT-----AC 791	
Db	579	TTACACCTGGACGCTTCATTTTTCATATTCATACAGTCAGTATCAATCTGGAAAGATTTCCAGAC	638
QY	792	ATTAAGAATAGTCATCTTGGGCTGGTCCCTCGGCTCGTGTGATGCTATCTGCTACTC	851
Db	639	ATTAAGAATAGTCATCTTGGGCTGGTCCCTCGGCTCGTGTGATGCTATCTGCTACTC	698
QY	852	GGGAATCTTAAACCTCTGCTCGGTTCGAAATGAGAAGAGAGGACAGAGGCTGTGAG	911
Db	699	GGGAATCTTAAACCTCTGCTCGGTTCGAAATGAGAAGAGAGGACAGAGGCTGTGAG	758
QY	912	GCTTATCTTACCATCATGATGTTTATTTTCTCTCTGGGCTCCCTTACAACATTTGCT	971
Db	759	GCTTATCTTACCATCATGATGTTTATTTTCTCTCTGGGCTCCCTTACAACATTTGCT	818
QY	972	TCTCTTGAAACACCTTCCAGGAATCTTTGGGCTGAATAATTGCATAGCTCTAACAGTT	1031
Db	819	TCTCTTGAAACACCTTCCAGGAATCTTTGGGCTGAATAATTGCATAGCTCTAACAGTT	878
QY	1032	GGNCAAGCTATCGAGGTGACAGAGACTTTGGGATGACGCATCTGTCATCAACCCCAT	1091
Db	879	GGNCAAGCTATCGAGGTGACAGAGACTTTGGGATGACGCATCTGTCATCAACCCCAT	938
QY	1092	CATCTATGCTTTGTGCGGGAGAGTTCCAGAACTACTCTTAGTCTTCATCCAAAGCA	1151
Db	939	CATCTATGCTTTGTGCGGGAGAGTTCCAGAACTACTCTTAGTCTTCATCCAAAGCA	998
QY	1152	CATTCGCCAAACGCTTCTGCAAAATGCTTCTTATTTTCCAGCAAGAGGCTCCCGACGAGC	1211
Db	999	CATTGCCAAACGCTTCTGCAAAATGCTTCTTATTTTCCAGCAAGAGGCTCCCGACGAGC	1058
QY	1212	AGGCTCAGTTTACCCCGATCCACTGGGAGCAGGAAATATCTGTGGGCTTTGTGACAGG	1271
Db	1059	AGGCTCAGTTTACCCCGATCCACTGGGAGCAGGAAATATCTGTGGGCTTTGTGACAGG	1118

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QY 1272 ACTCAAGTGGGCTGGTGACCCAGTCAGAGGTGTGCACATGGCTTAGTTTTCATACACAGC 1331
Db 1119 ACTCAAGTGGGCTGGTGACCCAGTCAGAGGTGTGCACATGGCTTAGTTTTCATACACAGC 1178
QY 1332 CTGGGCTGGGGTGG--TTGGGAGGTCCTTTTAAAGGAAGTACTGTTATAGAGGT 1388
Db 1179 CTGGGCTGGGGTGGGGTGGGAGAGGTCCTTTTAAAGGAAGTACTGTTATAGAGGT 1238
QY 1389 CTAAAGTATCATCCATTTATTTGGCATCTGTTTAAAGTAGATTAGATC 1435
Db 1239 CTAAAGTATCATCCATTTATTTGGCATCTGTTTAAAGTAGATTAGATC 1285

RESULT 8
US-08-724-984A-3
: Sequence 3, Application US/08724984A
: Patent No. 6388055
: GENERAL INFORMATION:
: APPLICANT: Derk Bergsma, Mary Brawner, and Usman Shabon
: TITLE OF INVENTION: No. 6388055el Mouse Genomic Clone of the CC-
: TITLE OF INVENTION: CKR5 Receptor
: NUMBER OF SEQUENCES: 5
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: SmithKline Beecham Corporation
: STREET: 709 Swedeland Road, P.O. Box 1539
: CITY: King of Prussia
: STATE: PA
: COUNTRY: USA
: ZIP: 19406-0939
: COMPUTER READABLE FORM:
: MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 Mb STORAGE
: COMPUTER: IBM 486
: OPERATING SYSTEM: WINDOWS FOR WORKGROUPS
: SOFTWARE: MICROSOFT WORD
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/724,984A
: FILING DATE: October 3, 1996
: CLASSIFICATION: 800
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER:
: FILING DATE:
: ATTORNEY/AGENT INFORMATION:
: NAME: William T. Han
: REGISTRATION NUMBER: 34,344
: REFERENCE/DOCKET NUMBER: ATG50023
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 610 270 5024
: TELEFAX: 610 270 5090
: INFORMATION FOR SEQ ID NO: 3:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 1059
: TYPE: Nucleic Acid
: STRANDEDNESS: Single
: TOPOLOGY: Linear
: ANTI-SENSE: NO
: US-08-724-984A-3

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Query Match	68.3%;	Score 985;	DB 4;	Length 1059;
Best Local Similarity	97.0%;	Pred. No. 2e-274;		
Matches 1027; Conservative	0;	Mismatches	0;	Indels 32; Gaps 1;
<hr/>				
QY	240	ATGGATTATCAAGTGTGAAGTCCTCATGACATCAATTTATTATACATCGAGCCCTGC	299	
Dd	1	ATGGATTATCAAGTGTGAAGTCCTCATGACATCAATTTATTATACATCGAGCCCTGC	60	
<hr/>				
QY	300	CAAAAATCAATGTGAAGCAAATCGAGCCGCCCTCGCTCCTACTCACTGTGTG	359	
Dd	61	CAAAAATCAATGTGAAGCAAATCGAGCCGCCCTCGCTCCTACTCACTGTGTG	120	
<hr/>				
QY	360	TTCATCTTTGGTTTTTGCGGCAAGATCGCTGGTTCATCTCATCTGATTAATCTGCAAAAG	419	
Dd	121	TTCATCTTTGGTTTTTGCGGCAAGATCGCTGGTTCATCTCATCTGATTAATCTGCAAAAG	180	

; Sequence 8, Application US/09517605
; Patent No. 6391567
; GENERAL INFORMATION:
; APPLICANT: Littman, Dan R.
; APPLICANT: Kwon, Douglas S.
; APPLICANT: Van Kooyk, Ivette
; APPLICANT: Gelitenbeck, Theo
; TITLE OF INVENTION: METHODS OF USING A FACILITATOR OF RETROVIRAL ENTRY INTO
; TITLE OF INVENTION: CELLS
; FILE REFERENCE: 1049-1-017
; CURRENT APPLICATION NUMBER: US/09/517,605
; CURRENT FILING DATE: 2000-03-02
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 8
; LENGTH: 1059
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-517-605-8

Query Match 56.2%; Score 954.6; DB 4; Length 1059;
Best Local Similarity 95.2%; Pred. No. 1.2e-265;
Matches 1008; Conservative 0; Mismatches 19; Indels 32; Gaps 1;

QY 240 ATGGATTATCAAGTGTCAAGTCCAACTATGATGATCAATTAATATATACATCGAGCCCTGC 299
DB 1 ATGGATTATCAAGTGTCAAGTCCAACTATGATGATCAATTAATATATACATCGAGCCCTGC 60
QY 300 CAAAATCAATGAGCAAAATCGAGCCCGCTCCGCTCGGCTCTACTCTACTCTGGTG 359
DB 61 CAAAATCAATGAGCAAAATCGAGCCCGCTCCGCTCGGCTCTACTCTACTCTGGTG 120
QY 360 TTCACTCTTGGTTTGGGCAACATGCTGCTCATCTCTCTCACTCTCACTCTGATTAACGCAAAAGG 419
DB 121 TTCACTCTTGGTTTGGGCAACATGCTGCTCATCTCTCTCACTCTCACTCTGATTAACGCAAAAGG 180
QY 420 CTGAAGAGCATGATGATCATCTACTCTGCTCAACCTGGCCATCTCTGACCTGTTTTCCTT 479
DB 181 CTGAAGAGCATGATGATCATCTACTCTGCTCAACCTGGCCATCTCTGACCTGTTTTCCTT 240
QY 480 CTACTCTCCCTCTGGGCTCACTATGCTGCGCCGAGTGGGACCTTTGGAATACATG 539
DB 241 CTACTCTCCCTCTGGGCTCACTATGCTGCGCCGAGTGGGACCTTTGGAATACATG 300
QY 540 TGTCAACTCTTGACAGGGCTCTATTTATAGGCTCTCTCTCTGGAATCTCTTTCATCATC 599
DB 301 TGTCAACTCTTGACAGGGCTCTATTTATAGGCTCTCTCTCTGGAATCTCTTTCATCATC 360
QY 600 CTCCTGCAATCATGATGATGATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 659
DB 361 CTCCTGCAATCATGATGATGATGATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 420
QY 560 AGGCTGACCTTTGGGCTGGTGCACAGTGTGATCATCTGCTGCTGCTGCTGCTGCTGCTGCT 719
DB 421 AGGCTGACCTTTGGGCTGGTGCACAGTGTGATCATCTGCTGCTGCTGCTGCTGCTGCTGCT 480
QY 720 CTCCTGCAATCATCTTACCAGATCTCAAAAGAGTCTTCAATTAACCTGCTGCTGCTGCT 779
DB 481 CTCCTGCAATCATCTTACCAGATCTCAAAAGAGTCTTCAATTAACCTGCTGCTGCTGCT 540
QY 780 CAATTTCCAT-----ACATTAAGATGATCATC 807
DB 541 CAATTTCCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 600
QY 808 TTGGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 867
DB 601 TTGGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 660
QY 868 CTGCT 927
DB 661 CTGCT 720
QY 928 ATGATTTGTTATTTTCTTCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 987

DB 721 ATGATTTGTTATTTTCTTCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 780
QY 988 CAGGAATTTTGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1047
DB 781 CAGGAATTTTGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 840
QY 1048 GTGACAGAGACTCTTGGGATGACGACTGCTGATCAACCCCACTCACTATGCTTGTCT 1107
DB 841 GTGACAGAGACTCTTGGGATGACGACTGCTGATCAACCCCACTCACTATGCTTGTCT 900
QY 1108 GGGGAGAGTTTCAGAACTACCTCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1167
DB 901 GGGGAGAGTTTCAGAACTACCTCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 960
QY 1168 TGCAAATCTGCTTCTATTTTCCAGAGAGCTCCGAGGAGCAAGCTGCTGCTGCTGCTGCT 1227
DB 961 TGCAAATCTGCTTCTATTTTCCAGAGAGCTCCGAGGAGCAAGCTGCTGCTGCTGCTGCT 1020
QY 1228 CGATCCACTGGGAGCAGGAGAAATATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1266
DB 1021 CGATCCACTGGGAGCAGGAGAAATATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1059

RESULT 12
US-08-833-752-1
; Sequence 1, Application US/08833752
; Patent No. 6448375
; GENERAL INFORMATION:
; APPLICANT: SAMSON, MICHEL
; APPLICANT: PARMANTIER, MARC
; APPLICANT: VASSART, GILBERT
; APPLICANT: LIBERT, FREDERICK
; TITLE OF INVENTION: ACTIVE AND INACTIVE CC-CHEMOKINES RECEPTOR
; TITLE OF INVENTION: AND NUCLEIC ACID MOLECULES ENCODING SAID RECEPTOR
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Knobb, Martens, Olson & Bear
; STREET: 620 Newport Center Drive 16th Floor
; CITY: Newport Beach
; STATE: CA
; COUNTRY: U.S.A.
; ZIP: 92660
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/833,752
; FILING DATE: 9-APR-1997
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Altman, Daniel E
; REGISTRATION NUMBER: 34,115
; REFERENCE/DOCKET NUMBER:
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 792 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 240..791
; US-08-833-752-1

Query Match 54.9%; Score 792; DB 4; Length 792;
Best Local Similarity 100.0%; Pred. No. 8.3e-219;
Matches 792; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAATTCCTCCCAACAGAGCCAAAGCTCTCCATCTAGTGCAGAGGAGTACAGCAAACT 60


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Db 1212 ACACACAGTATCATTTCTGAGAGAGTTTCCAAACATTAAGATGGTCACTCTGAGCCGGA 1271
QY 818 TCTGCGCCTGCTTGTCATGTCATCTGCTACTCGGGAATCCTAAAACCTCTGCTCGGT 877
Db 1272 TCTGCGCCTGCTACTGTCATGATCATCTGCTACTCAGGAATCTCCACACCCCTGTTGCT 1331
QY 878 GTCCAAATGACAGAGAGGACAGGCGTGTGAGGCTTATCTTCCATCATCATGATGTTT 937
Db 1332 GTAGGAATGAGAGAGAGGACAGGCGTGTGAGGCTTATCTTGGCCATCATGATGTTCT 1391
QY 938 ATTCTCTCTTCTGGGCTCCCTACACATTTGCTCTCTGTAACACCTTCCAGGAATCT 997
Db 1392 ACTTCTCTCTGAGCTCCCTACACATTTGCTCTCTCTGTAACACCTTCCAGGAATCT 1451
QY 998 TTGGCCTGGAATATGCTAGTCTCTACAGGTTGACCAAGCTATGCAAGGTGACAGAGA 1057
Db 1452 TTGGACTGAATATGCTAGTCTCTATAGACTAGACAGGCCATGACAGCAACAGAGA 1511
QY 1058 CTCTTGGATGACGCACTGCTGATCAACCCCATCATCTATGCTCTGTTGGGGAGAGT 1117
Db 1512 CTCTTGGATGACACACTGCTGCTTAACCCCTGCTCATCTATGCTCTTGTGGAGAGA 1571
QY 1118 TCAGAACTACTCTTAGTCTTCTTCCAAAGACATTCGCCAAACGCTTCTGCAATGCT 1177
Db 1572 TCGGAGTATCTCTAGTCTTCTTCCGAAACACATTTGCAACGCTTTTGCACACGCT 1631
QY 1178 GTTCTATTTTCCAGAGAGGCTCCGAGGACAGCTAGTCTAGTTACACCCGATCCAGT 1237
Db 1632 GTTCAATTTTCCAGAGAGCAATCCTGATGCTGTAGCTCAGTCTATACCCGATCCAG 1691
QY 1238 GGGAGCAGGAATATCTGGGCTTGTGACACGCACTCAAGTGGGCTGGTGACCCAGTCA 1297
Db 1692 GAGACATGAGTTTCTACTGTTATGA -----CGTGGT 1727
QY 1298 GAGTGTGCAATAGGCTTATGTTTTCATACACAGCTGGGCTGGGGGTGTGGAGGCT 1357
Db 1728 GACTTTTGTATCAGCTAGTTTCTATGCACTT-----GGGAGTAGGAATGGTTC 1780
QY 1358 TTTTAAAGAGTCTAGTTATAGAGGCTCTAAGATTCATCCATTTATTTGGCATG 1417
Db 1781 TTTTAAAGAAATAGTATCATAGAGGCCAAGATACATGATCTTTTGTATATTA 1840
QY 1418 TTTAAG 1424
Db 1841 TTTTAG 1847

RESULT 14
US-08-450-393A-3
; Sequence 3, Application US/08450393A
; Patent No. 5707815
; GENERAL INFORMATION:
; APPLICANT: Charo, Israel
; APPLICANT: Coughlin, Shaun
; TITLE OF INVENTION: MAMMALIAN MONOCYTE CHEMOATTRACTANT
; TITLE OF INVENTION: PROTEIN RECEPTORS
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Cooley Godward Castro Huddleson & Tatum
; STREET: 5 Palo Alto Square
; CITY: Palo Alto
; STATE: California
; COUNTRY: USA
; ZIP: 94306-2155
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/450,393A
; FILING DATE: May 25, 1995
; CLASSIFICATION: 424
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; ATTORNEY/AGENT INFORMATION:
; NAME: Cseri, Luand
; REGISTRATION NUMBER: 31,822
; REFERENCE/DOCKET NUMBER: UCAL-237/02US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-843-5165
; TELEFAX: 415-8857-0663
; TELEX: 380816COOLEYPA
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1979 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 81..1160
; US-08-450-393A-3

Query Match 47.4%; Score 683.4; DB 1; Length 1979;
Best Local Similarity 80.0%; Pred. No. 2.8e-187;
Matches 825; Conservative 0; Mismatches 186; Indels 20; Gaps 1;

QY 277 ATTATATATACATCGAGCGCTGCCAAAAATCAATGTGAAGCAAAATCGACGCCGCTCC 336
Db 154 ATTATGATTACGGTCTCCCTGTCAATAATTGACGTGAAGCAAAATTTGGGCCCAACTCC 213
QY 337 TGCCCTCGCTCTACCTACCTGGTGTTCATCTTTGTTTGGGCAACATGTGGTCTATCC 396
Db 214 TGCCCTCGCTCTACCTACCTGGTGTTCATCTTTGTTTGGGCAACATGTGGTCTATCC 273
QY 337 TCATCTCTGATTAACCTGCAAAAGGCTGAAGAGCATGACTGACATCTACCTGCTCAACCTGG 456
Db 274 TCATCTTAATAACCTGCAAAAGGCTGAAGAGCATGACTGACATCTACCTGCTCAACCTGG 333
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RESULT 15

US-08-446-669-3
; Sequence 3, Application US/08446669
; Patent No. 6132987
; GENERAL INFORMATION:
; APPLICANT: Charo, Israel
; APPLICANT: Coughlin, Shaun
; TITLE OF INVENTION: MAMMALIAN MONOCYTE CHEMOATTRACTANT
; TITLE OF INVENTION: PROTEIN RECEPTORS
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Cooley Godward Castro Huddleson & Tatum
; STREET: 5 Palo Alto Square
; CITY: Palo Alto
; STATE: California
; COUNTRY: USA
; ZIP: 94306-2155
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/446,669
; FILING DATE: May 25, 1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Neeley, Richard
; REGISTRATION NUMBER: 30,092
; REFERENCE/DOCKET NUMBER: UCAL-237/01US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-843-5000
; TELEFAX: 415-857-0663
; TELEX: 380816CooleyPPA
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1979 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
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; LOCATION: 81..1160
US-08-446-669-3

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Job time : 82 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: June 8, 2003, 08:51:52 ; Search time 223 Seconds
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Perfect score: 1442
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Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 870385 seqs, 699768693 residues
Total number of hits satisfying chosen parameters: 1740770

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications, NA:*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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5	1382.8	95.9	1477	10	US-09-938-719-2
6	1382.8	95.9	1477	10	US-09-939-226-2
7	1382.8	95.9	1477	10	US-09-938-703-2
8	1375.2	95.4	143068	9	US-09-967-768A-316
9	1302	90.3	1376	9	US-10-086-814-2
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21	1117	77.5	1225	10	US-09-813-653-14	Sequence 14, Appli
22	1115.4	77.4	1225	10	US-09-813-653-16	Sequence 16, Appli
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ALIGNMENTS

RESULT 1
US-09-938-719-3
; Sequence 3, Application US/0938719
; Patent No. US20020106742A1
; GENERAL INFORMATION:
; APPLICANT: SAMSON, MICHEL
; PARMENTIER, MARC
; VASSART, GILBERT
; LIBERT, FREDERICK

TITLE OF INVENTION: ACTIVE AND INACTIVE CC-CHEMOKINES RECEPTOR
AND NUCLEIC ACID MOLECULES ENCODING SAID RECEPTOR

NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESSEE: Knobbe, Martens, Olson & Bear
STREET: 620 Newport Center Drive 16th Floor
CITY: Newport Beach
STATE: CA
COUNTRY: U.S.A.
ZIP: 92660

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION NUMBER: US/09/938,719
APPLICATION DATE: 24-Aug-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/626,939
FILING DATE: 27-JULY-2000
ATTORNEY/AGENT INFORMATION:
NAME: Altman, Daniel E
REGISTRATION NUMBER: 34,115
REFERENCE FOR SEQ ID NO: 3:
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 1442 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)

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FEATURE:
NAME/KEY: CDS
LOCATION: 240..884
SEQUENCE DESCRIPTION: SEQ ID NO: 3:
US-09-938-719-3

Query Match      100.0%; Score 1442; DB 10; Length 1442;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1442; Conservativity 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 2
US-09-939-226-3
; Sequence 3, Application US/09939226
; Patent No. US20020110805A1
GENERAL INFORMATION:
APPLICANT: SAMSON, MICHEL
VASSART, GILBERT
LIBERT, FREDERICK
TITLE OF INVENTION: ACTIVE AND INACTIVE CC-CHEMOKINES RECEPTOR
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESSEE: Knobbe, Martens, Olson & Bear
STREET: 620 Newport Center Drive 16th Floor
CITY: Newport Beach
STATE: CA
COUNTRY: U.S.A.
ZIP: 92660
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/939,226
FILING DATE: 24-Aug-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/626,939
FILING DATE: 2000-07-27
ATTORNEY/AGENT INFORMATION:
NAME: Altman, Daniel E
REGISTRATION NUMBER: 34,115
REFERENCE/DOCKET NUMBER: <Unknown>
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INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 1442 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
FEATURE:
NAME/KEY: CDS
LOCATION: 240..884
SEQUENCE DESCRIPTION: SEQ ID NO: 3:
US-09-939-226-3

Query Match 100.0%; Score 1442; DB 10; Length 1442;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1442; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 901 AGGCTGTGAGGCTTATCTTCAACATCATGATGTTTATTTTCTCTCTGGGCTCCCTAC 960
DB 901 AGGCTGTGAGGCTTATCTTCAACATCATGATGTTTATTTCTCTCTGGGCTCCCTAC 960
QY 961 AACATGTCCTCTCTCGTGAACACCTTCCAGGATCTCTTGGCTGATATGTCAGTAGC 1020
DB 961 AACATGTCCTCTCTCGTGAACACCTTCCAGGATCTCTTGGCTGATATGTCAGTAGC 1020
QY 1021 TCTAACAGGTTGACCAAGCTATGACGCTGACAGAGACTCTTGGATGACGCACTGCTGC 1080
DB 1021 TCTAACAGGTTGACCAAGCTATGACGCTGACAGAGACTCTTGGATGACGCACTGCTGC 1080
QY 1081 ATCAACCCCATCATCTATGCTTGTGCGGAGAGAGTTTCAGAAACTACCTCTAGCTTC 1140
DB 1081 ATCAACCCCATCATCTATGCTTGTGCGGAGAGAGTTTCAGAAACTACCTCTAGCTTC 1140
QY 1141 TTCCAAAAGACACATTCGCAACGCTTCTGCAATGCTTCTATTTTCCAGCAAGGCT 1200
DB 1141 TTCCAAAAGACACATTCGCAACGCTTCTGCAATGCTTCTATTTTCCAGCAAGGCT 1200
QY 1201 CCCGAGCGAGCAAGCTCAGTTTACACCCGATCCACTGGGAGCAGGAAATATCTGTGGC 1260
DB 1201 CCCGAGCGAGCAAGCTCAGTTTACACCCGATCCACTGGGAGCAGGAAATATCTGTGGC 1260
QY 1261 TTGTGACAGGACTCAAGTGGGCTGGTGGCTGGTGGCTGGTGGCTGGCTGGCTGGCT 1320
DB 1261 TTGTGACAGGACTCAAGTGGGCTGGTGGCTGGTGGCTGGTGGCTGGCTGGCTGGCT 1320
QY 1321 TCATACACAGCTGGGCTGGGCTGGGCTGGGCTGGGCTGGGCTGGGCTGGGCTGGGCT 1380
DB 1321 TCATACACAGCTGGGCTGGGCTGGGCTGGGCTGGGCTGGGCTGGGCTGGGCTGGGCT 1380
QY 1381 TAGAGGCTTAAGATTCATCCATTTATTTGGCATCTGTTTAAAGAGAGTACTGTTA 1440
DB 1381 TAGAGGCTTAAGATTCATCCATTTATTTGGCATCTGTTTAAAGAGAGTACTGTTA 1440
QY 1441 TC 1442
DB 1441 TC 1442

RESULT 3
US-09-938-703-3
Sequence 3, Application US/09938703
Patent No. US20020110870A1
GENERAL INFORMATION:
APPLICANT: SAMSON, MICHEL
PARMENTIER, MARC
VASSART, GILBERT
LIBERT, FREDERICK
TITLE OF INVENTION: ACTIVE AND INACTIVE CC-CHEMOKINES RECEPTOR
AND NUCLEIC ACID MOLECULES ENCODING SAID RECEPTOR
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESSEE: Knobbe, Martens, Olson & Bear
STREET: 620 Newport Center Drive 16th Floor
CITY: Newport Beach
STATE: CA
COUNTRY: U.S.A.
ZIP: 92660
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/938,703
FILING DATE: 24-Aug-2001
CLASSIFICATION: <Unknown>

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, PRIOR APPLICATION DATA:
, APPLICATION NUMBER: 09/626,939
, FILING DATE: 2000-07-27
, ATTORNEY/AGENT INFORMATION:
, NAME: Altman, Daniel E
, REGISTRATION NUMBER: 34,115
, REFERENCE/DOCKET NUMBER: <Unknown>
, INFORMATION FOR SEQ ID NO: 3:
,
, SEQUENCE CHARACTERISTICS:
, LENGTH: 1442 base pairs
, TYPE: nucleic acid
, STRANDEDNESS: single
, TOPOLOGY: linear
, MOLECULE TYPE: DNA (genomic)
, FEATURE:
, NAME/KEY: CDS
, LOCATION: 240..884
, SEQUENCE DESCRIPTION: SEQ ID NO: 3:
US-09-938-703-3

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Db	721	TCCAGGAATCATCTTTACAGATCTCAAAAGAAGGTCTTCATTACACCTGCAGCTCTC	780
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Db	781	ATTTTCCATCATTAAGAATAGTCACTTGGGGCTGGTCTCGCTCGCTGTCATGGTC	840
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QY	901	AGGCTGTGAGGCTTATCTTCAACATCATGATGTTTATTTTCTCTTGGGCTCCCTAC	960
Db	901	AGGCTGTGAGGCTTATCTTCAACATCATGATGTTTATTTTCTCTTGGGCTCCCTAC	960
QY	961	AACATTTGCCTTCTCTGTAACACCTTCCAGGAATTCCTTGGCTGAATAATTCAGTAGC	1020
Db	961	AACATTTGCCTTCTCTGTAACACCTTCCAGGAATTCCTTGGCTGAATAATTCAGTAGC	1020
QY	1021	TCTACAGGTTGACCAAGCTATCAGGTTGACAGAGACTCTTGGGATGAAGCACTCTGTC	1080
Db	1021	TCTACAGGTTGACCAAGCTATCAGGTTGACAGAGACTCTTGGGATGAAGCACTCTGTC	1080
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QY	1141	TTCAAAAAGCACATTGCCAAACGGTTCTGCAAAATGCTTTCTATTTTCCAGCAAGAGCT	1200
Db	1141	TTCAAAAAGCACATTGCCAAACGGTTCTGCAAAATGCTTTCTATTTTCCAGCAAGAGCT	1200
QY	1201	CCGAGGAGCAGCTCAGTTTACCCCGATCCACTGGGAGCAGGAATAATCTGTGGGC	1260
Db	1201	CCGAGGAGCAGCTCAGTTTACCCCGATCCACTGGGAGCAGGAATAATCTGTGGGC	1260
QY	1261	TTGTGACACGAGCTCAAGTGGGCTGTGTGACCCAGTCAGAGTTGTGCATGGCTTAAGTT	1320
Db	1261	TTGTGACACGAGCTCAAGTGGGCTGTGTGACCCAGTCAGAGTTGTGCATGGCTTAAGTT	1320
QY	1321	TCAATACAGCCTGGGCTGGGGGTGTGGAGGTCTTTTTTAAAGGAAGTTCATGTTA	1380
Db	1321	TCAATACAGCCTGGGCTGGGGGTGTGGAGGTCTTTTTTAAAGGAAGTTCATGTTA	1380
QY	1381	TGAGGGTCTAAGATCATCCATTATTTGGCATCTGTTTAAAGTAGATTAGATCCGAAT	1440
Db	1381	TGAGGGTCTAAGATCATCCATTATTTGGCATCTGTTTAAAGTAGATTAGATCCGAAT	1440
QY	1441	TC 1442	
Db	1441	TC 1442	

QY 721 TCCAGGAATCATCTTTACCAGATCTCAAAAGAAGGTCTTCATTACCTGCAGCTCTC 780

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; LENGTH: 1477
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 1377..1384, 1385
; OTHER INFORMATION: n is a or g or c or t/u
US-09-759-841-1

Query Match          95.9%; Score 1382.8; DB 10; Length 1477;
Best Local Similarity 97.4%; Pred. No. 0;
Matches 1439; Conservative 0; Mismatches 3; Indels 35; Gaps 2;

QY 1 GAATTCCTCCCAAGAGCCAGCTCTCCATCTAGTGGACAGGGAAGCTAGCAGCAAACT 60
Db 1 GAATTCCTCCCAAGAGCCAGCTCTCCATCTAGTGGACAGGGAAGCTAGCAGCAAACT 60
QY 61 TCCTTCTCACTACAAACTTCATTTGCTGGCCAAAAGAGAGTTAATCAATGTAGACATC 120
Db 61 TCCTTCTCACTACAAACTTCATTTGCTGGCCAAAAGAGAGTTAATCAATGTAGACATC 120
QY 121 TAGTAGGCAATTAAGCACTATGATGATATAAAACAGTTTGCATTCATGGAGGCAACT 180
Db 121 TAGTAGGCAATTAAGCACTATGATGATATAAAACAGTTTGCATTCATGGAGGCAACT 180
QY 181 AATATCACTTAGGACTTTATAAAGATCACTTTTATTTATGACAGGGTGGAAACAAG 240
Db 181 AATATCACTTAGGACTTTATAAAGATCACTTTTATTTATGACAGGGTGGAAACAAG 240
QY 241 TGGATTATCAAGTGTCAAGTCCCAATCTATGACATCAATTTATATACATCGAGCCCTGCC 300
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Db 301 AAAAATCAATGTGAAGCAAAATCGCAGCCGCTCTGCTCCGCTCTACTCTACTGGTGT 360
QY 361 TCATCTTTGGTTTGTGGGCAACATGCTGTCTCATCTCATCTGATTAACATGCAAAAGC 420
Db 361 TCATCTTTGGTTTGTGGGCAACATGCTGTCTCATCTCATCTGATTAACATGCAAAAGC 420
QY 421 TGAAGAGCATGACATGACATACCTGCTCAACCTGGCCATCTCTGACCTGTTTTCTCTTC 480
Db 421 TGAAGAGCATGACATGACATACCTGCTCAACCTGGCCATCTCTGACCTGTTTTCTCTTC 480
QY 481 TTACTGCTCCCTCTGGCTCAGTATGCTGCGCCGACAGTGGGACTTTGGAATACAAATGT 540
Db 481 TTACTGCTCCCTCTGGCTCAGTATGCTGCGCCGACAGTGGGACTTTGGAATACAAATGT 540
QY 541 GTCACTCTTGACAGGCTCTAATTTATAGGCTTCTCTGGAATCTTCTTCATCATCC 600
Db 541 GTCACTCTTGACAGGCTCTAATTTATAGGCTTCTCTGGAATCTTCTTCATCATCC 600
QY 601 TCCTGACATCGATAGTACGTGGCTGTCGTCGTCACGCTGTGTTTCTGTTTAAAGCCAGGA 660
Db 601 TCCTGACATCGATAGTACGTGGCTGTCGTCGTCACGCTGTGTTTCTGTTTAAAGCCAGGA 660
QY 661 CGGTACCTTTGGGCTGGTGACAGTGTGATCACTTGGGTGGGTGGCTGCTGTTTGGCTCTC 720
Db 661 CGGTACCTTTGGGCTGGTGACAGTGTGATCACTTGGGTGGGTGGCTGCTGTTTGGCTCTC 720
QY 721 TCCAGGAATCATCTTTACAGATCTCAAAAGAGCTTTCATTTACACCTTGCAGCTCTC 780
Db 721 TCCAGGAATCATCTTTACAGATCTCAAAAGAGCTTTCATTTACACCTTGCAGCTCTC 780
QY 781 ATTTTCCAT-----ACATTAAGATAGTCACT 808
Db 781 ATTTTCCATAGTCACTAATCTGGAAGATTTTCCAGACATTAAGATAGTCACT 840
QY 809 TGGGCTGCTGCTCCGCTCTGTCATGATGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 868
Db 841 TGGGCTGCTGCTCCGCTCTGTCATGGGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 900
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QY 869 TGCTTCGGTGTGCAAAATGAGAAGAGAGGACAGAGGCTGTGAGGCTTATCTTCACCATCA 928
Db 901 TGCTTCGGTGTGCAAAATGAGAAGAGAGGACAGAGGCTGTGAGGCTTATCTTCACCATCA 960
QY 929 TGATTGTTTATTTCTCTCTGCGCTCCCTACACANTGCTCTCTCTGACACCTTCC 988
Db 961 TGATTGTTTATTTCTCTCTGCGCTCCCTACACANTGCTCTCTCTGACACCTTCC 1020
QY 989 AGGAATCTTTGGCCTGAATAATTCAGTAGTCTTAACAGGTTGGACCAAGCTATGCGG 1048
Db 1021 AGGAATCTTTGGCCTGAATAATTCAGTAGTCTTAACAGGTTGGACCAAGCTATGCGG 1080
QY 1049 TGACAGAGACTCTTGGGATGAGCGACTGCTGCATCAACCCCATCATCTATGCTTTGCG 1108
Db 1081 TGACAGAGACTCTTGGGATGAGCGACTGCTGCATCAACCCCATCATCTATGCTTTGCG 1140
QY 1109 GGGAGAAGTTCAGAACTACCTCTTAGTCTTCTTCCAAAAGACATTCGCAACGCTTCT 1168
Db 1141 GGGAGAAGTTCAGAACTACCTCTTAGTCTTCTTCCAAAAGACATTCGCAACGCTTCT 1200
QY 1169 GCAAACTGTTCTTATTTCCAGCAAGAGCTCCCGAGCGAGCAAGCTCAGTTTACACC 1228
Db 1201 GCAAACTGTTCTATTTTCCAGCAAGAGCTCCCGAGCGAGCAAGCTCAGTTTACACC 1260
QY 1229 GATCCACTGGGAGCAGGAGATATCTGTGGGCTTGTGACACGACTCAAGTGGGCTGG 1288
Db 1261 GATCCACTGGGAGCAGGAGATATCTGTGGGCTTGTGACACGACTCAAGTGGGCTGG 1320
QY 1289 ACCCAGTTCAGAGTGTGACATGCTTATTTTATACACAGCTGGGCTGGGCTGGTT 1348
Db 1321 ACCCAGTTCAGAGTGTGACATGCTTATTTTATACACAGCTGGGCTGGGCTGGTT 1380
QY 1349 GG---GAGGCTTTTTTAAAGAGAGTACTCTTATAGAGGGTCTAAGATTCATCCATT 1405
Db 1381 TGGNAGGCTTTTTTAAAGAGAGTACTCTTATAGAGGGTCTAAGATTCATCCATT 1440
QY 1406 ATTTGGCATCTGTTTAAAGTAGATTAGATCCGAATTC 1442
Db 1441 ATTTGGCATCTGTTTAAAGTAGATTAGATCCGAATTC 1477

RESULT 5
US-09-938-719-2
; Sequence 2, Application US/09938719
; Patent No. US2020106742A1
; GENERAL INFORMATION:
; APPLICANT: SAMSON, MICHEL
; VASSART, GILBERT
; LIBERT, FREDERICK
; TITLE OF INVENTION: ACTIVE AND INACTIVE CC-CHEMOKINES RECEPTOR
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Knobbe, Martens, Olson & Bear
; STREET: 620 Newport Center Drive 16th Floor
; CITY: Newport Beach
; STATE: CA
; COUNTRY: U.S.A.
; ZIP: 92660
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/938,719
; FILING DATE: 24-Aug-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/626,939
; FILING DATE: 27-JULY-2000
; ATTORNEY/AGENT INFORMATION:
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NAME: Altman, Daniel E
REGISTRATION NUMBER: 34,115
REFERENCE/DOCKET NUMBER: <Unknown>
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 1477 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
FEATURE:
NAME/KEY: CDS
LOCATION: 240..1295
SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-09-938-719-2

Query Match          95.9%; Score 1382.8; DB 10; Length 1477;
Best Local Similarity 97.4%; Pred. No. 0;
Matches 1439; Conservative 0; Mismatches 3; Indels 35; Gaps 2;

QY 1 GAATTCCTCCACAGAGCAAGCTCTCCATCTAGTGGACAGGGAAGCTAGCAGCAAAACCT 60
DB 1 GAATTCCTCCACAGAGCAAGCTCTCCATCTAGTGGACAGGGAAGCTAGCAGCAAAACCT 60
QY 61 TCCCTTCACACAAACCTCAATGCTTGGCCAAAGAGAGTAAATCAATGTAGACATC 120
DB 61 TCCCTTCACACAAACCTCAATGCTTGGCCAAAGAGAGTAAATCAATGTAGACATC 120
QY 121 TATGTAGGCAATTAACCACTATTGATGATATAACAGCTTGCATTCATGGAGGCAACT 180
DB 121 TATGTAGGCAATTAACCACTATTGATGATATAACAGCTTGCATTCATGGAGGCAACT 180
QY 181 AAATACATCTAGGACTTTAAGAGATCACATTTTATATGACAGAGGTTGGAACAAGA 240
DB 181 AAATACATCTAGGACTTTAAGAGATCACATTTTATATGACAGAGGTTGGAACAAGA 240
QY 241 TGGATTATCAAGTGCAAGTCCCAATCTATGACATCAATTAATATACATCGAGCCCTGCC 300
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QY 301 AAAAATCAATGTGAAGCAATCGACGCCGCTCTCCCTCGCGCTCTACTCACTGGTGT 360
DB 301 AAAAATCAATGTGAAGCAATCGACGCCGCTCTCCCTCGCGCTCTACTCACTGGTGT 360
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DB 481 TTACTGTCCCTTCTGGGCTCAGTATGCTGCGGCCAGTGGGACTTTGGAATACAATGT 540
QY 541 GTCAACTCTTGACAGGCTCTATTTATAGGCTTCTCTCGGAATCTTCTTCATCATCC 600
DB 541 GTCAACTCTTGACAGGCTCTATTTATAGGCTTCTCTCGGAATCTTCTTCATCATCC 600
QY 601 TCGTGAATCGATAGGACCTGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 660
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QY 661 CGGTCACTTTGGGTTGGTGAAGTGTATCACTTGGGTTGGTGGTGGTGGTGGTGGTGGTGG 720
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QY 721 TCCAGGAATCATCTTTACAGATCTCAAAAGAGAGTCTTCATTCACCTGCAGCTCTC 780
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QY 781 ATTTCAT-----ACATTAAGATAGTCACT 808
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DB 781 ATTTCATATACAGTCACTATCAATTTCTGGAAGAAATTTCCAGACATTAAGATAGTCACT 840
QY 809 TGGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 868
DB 841 TGGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 900
QY 869 TGTTCGGTGTGCGAAATGAGAAGAGAGGACAGGCTGTGAGGCTTATCTTCACCATCA 928
DB 901 TGTTCGGTGTGCGAAATGAGAAGAGAGGACAGGCTGTGAGGCTTATCTTCACCATCA 960
QY 929 TGAATGTTTATTTCTTCTTGGGCTCCCTACAACTTGTCTTCTTCTTCTTCTTCTTCTTCT 988
DB 961 TGAATGTTTATTTCTTCTTGGGCTCCCTACAACTTGTCTTCTTCTTCTTCTTCTTCTTCT 1020
QY 989 AGGAATCTTTGGCTGCAATATTTGCAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1048
DB 1021 AGGAATCTTTGGCTGCAATATTTGCAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1080
QY 1049 TGACAGAGACTCTTGGGATGAGGCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1108
DB 1081 TGACAGAGACTCTTGGGATGAGGCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1140
QY 1109 GGGAGAAGTTCAGAACTACCTCTTGTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 1168
DB 1141 GGGAGAAGTTCAGAACTACCTCTTGTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 1200
QY 1169 GCAATCTGCTTCTTATTTCCAGCAAGAGGCTCCGAGGAGCAAGCTCAGTTTACACCC 1228
DB 1201 GCAATCTGCTTCTTATTTCCAGCAAGAGGCTCCGAGGAGCAAGCTCAGTTTACACCC 1260
QY 1229 GATCCACTGGGAGAGCAAGAAATATCTGTTGGGCTTGTGACACGAGCTCAAGTGGGCTGGTG 1288
DB 1261 GATCCACTGGGAGAGCAAGAAATATCTGTTGGGCTTGTGACACGAGCTCAAGTGGGCTGGTG 1320
QY 1289 ACCAGTTCAGAGTGTGACATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1348
DB 1321 ACCAGTTCAGAGTGTGACATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1380
QY 1349 GG---GAGTCTTTTAAAGAGAGTACTGTTATAGAGGCTCTAAGATTCATCCATTT 1405
DB 1381 TGGNNGAGTCTTTTAAAGAGAGTACTGTTATAGAGGCTCTAAGATTCATCCATTT 1440
QY 1406 ATTGGCATCTGTTTAAAGTAGATTAGATCCGAATTC 1442
DB 1441 ATTGGCATCTGTTTAAAGTAGATTAGATCCGAATTC 1477
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RESULT 6

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US-09-939-226-2
; Sequence 2, Application US/09939226
; Patent No. US20020110805A1
; GENERAL INFORMATION:
; APPLICANT: SAMSON, MICHEL
; VASSART, GILBERT
; PARMENTIER, MARC
; LIBERT, FREDERICK
; TITLE OF INVENTION: ACTIVE AND INACTIVE CC-CHEMOKINES RECEPTOR
; AND NUCLEIC ACID MOLECULES ENCODING SAID RECEPTOR
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Knobbe, Martens, Olson & Bear
; STREET: 620 Newport Center Drive 16th Floor
; CITY: Newport Beach
; STATE: CA
; COUNTRY: U.S.A.
; ZIP: 92660
; COMPUTER READABLE FORM:
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION DATA:
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Db	61	TCCCTTCACTACAAACTTCATTGCTTGGCCAAAAGAGAGTTAATCAATGTAGACATC	120
QY	121	TATGTAGGCAATTAAAAAAGCTATTGATGTATATAAACHAGTTTGCATTCATGGAGGCAACT	180
Db	121	TATGTAGGCAATTAAAAAAGCTATTGATGTATATAAACHAGTTTGCATTCATGGAGGCAACT	180
QY	181	AAATACATCTTAGGACTTTATAAAGATCACCTTTTATTTATGCACAGGTTGGAAACAAG	240
Db	181	AAATACATCTTAGGACTTTATAAAGATCACCTTTTATTTATGCACAGGTTGGAAACAAG	240
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Db	241	TGGATTACAAGTGTCAAGTCCAATCTATGACATCAATATTATACATCGAGGCGCTTGCC	300
QY	301	AAAAATCAATGTGAAGCAAAATCGACGCGCGCTCTCGCTCGGCTCTACTCACTGGTGT	360
Db	301	AAAAATCAATGTGAAGCAAAATCGACGCGCGCTCTCGCTCGGCTCTACTCACTGGTGT	360
QY	361	TCATCTTTGGTTTGTGGCAACATGCTGGTCAATCCCTCATCTGATAACTGCAAAAGGC	420
Db	361	TCATCTTTGGTTTGTGGCAACATGCTGGTCAATCCCTCATCTGATAACTGCAAAAGGC	420
QY	421	TGAAGAGCATGACTGACATCTACCTGCTCAACCTGGCCATCTGTGACCTGTTTTCCTTC	480
Db	421	TGAAGAGCATGACTGACATCTACCTGCTCAACCTGGCCATCTGTGACCTGTTTTCCTTC	480
QY	481	TTACTGTCCCTTCTCGGGCTCACTATGCTGGCCGCCAGTGGGACTTTGGAATAACAATGT	540
Db	481	TTACTGTCCCTTCTCGGGCTCACTATGCTGGCCGCCAGTGGGACTTTGGAATAACAATGT	540
QY	541	GTCAACTCTTGACAGGGCTCTATTTTATAGGCTCTCTCTGGAATCTTCTCATCATCC	600
Db	541	GTCAACTCTTGACAGGGCTCTATTTTATAGGCTCTCTCTGGAATCTTCTCATCATCC	600
QY	601	TCTGACAATCGATAGGTACCTGGCTGCTGCATCTGTGTTGCTTTTAAAGCCAGGA	660
Db	601	TCTGACAATCGATAGGTACCTGGCTGCTGCATCTGTGTTGCTTTTAAAGCCAGGA	660
QY	661	CGGTCAACCTTTGGGGTGTGACAAAGTGTGATCATTGGGTGGTGGCTGTGTTTCCGTCTC	720

ZIP: 92660
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/938,703
FILING DATE: 24-Aug-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/626,939
FILING DATE: 2000-07-27
ATTORNEY/AGENT INFORMATION:
NAME: Altman, Daniel E
REGISTRATION NUMBER: 34,115
REFERENCE/DOCKET NUMBER: <Unknown>
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 1477 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
FEATURE:
NAME/KEY: CDS
LOCATION: 240..1295
SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-09-938-703-2

Query Match 95.9%; Score 1382.8; DB 10; Length 1477;
Best Local Similarity 97.4%; Pred. No. 0;
Matches 1439; Conservative 0; Mismatches 3; Indels 35; Gaps 2;
QY 1 GAATCCCCCAACAGAGCAAGCTCTCCATCTAGTGACAGGAGGAGCTAGCAGCAACCT 60
DB 1 GAATCCCCCAACAGAGCAAGCTCTCCATCTAGTGACAGGAGGAGCTAGCAGCAACCT 60
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DB 61 TCCCTTCACACAACTTCATGCTGGCCAAAGAGAGTAAATCAATGAGATC 120
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DB 181 AAATACATCTAGGACTTTAATAAGATCATTATTTATGACAGAGGTGGAACAAGA 240
QY 241 TGGATTATCAAGTCAAGTCCATCTATGACATCAATATATATACATGAGGCGCTGC 300
DB 241 TGGATTATCAAGTCAAGTCCATCTATGACATCAATATATATACATGAGGCGCTGC 300
QY 301 AAAAATCAATGTGAAGCAATCGACGCCCTCTGCTCGCTCTACTCACTGGTGT 360
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DB 361 TCATCTTTGGTTTTGTGGCAACATGCTGGTCACTCCCTGATGAATGCAAAAGGC 420
QY 421 TGAAGACATGACTGACATCTACCTGCTCAACCTGGCCATCTGACCTGTTTTCTCTC 480
DB 421 TGAAGACATGACTGACATCTACCTGCTCAACCTGGCCATCTGACCTGTTTTCTCTC 480
QY 481 TTACTGTCCCTTTCTGGCTCATTGCTGCGGCCAGTGGGACTTTGGAATCAATGT 540
DB 481 TTACTGTCCCTTTCTGGCTCATTGCTGCGGCCAGTGGGACTTTGGAATCAATGT 540
QY 541 GTCAACTCTTGACAGGCTCTATTTATAGGCTTCTCTGGAATCTTCTTCATCATCC 600
DB 541 GTCAACTCTTGACAGGCTCTATTTATAGGCTTCTCTGGAATCTTCTTCATCATCC 600

QY 601 TCCTGCAATCGATAGTAGTACCTGGCTGTGCTCATCTGTGTGTTGCTTTAAAGCCAGGA 660
DB 601 TCCTGCAATCGATAGTAGTACCTGGCTGTGCTCATCTGTGTGTTGCTTTAAAGCCAGGA 660
QY 661 CGGTCACTTTGGGGTGGTGACAAAGTGTGATCATTGGGTGGTGGTGGTGGTGGTGGT 720
DB 661 CGGTCACTTTGGGGTGGTGACAAAGTGTGATCATTGGGTGGTGGTGGTGGTGGTGGT 720
QY 721 TCCAGGAACTCACTTTACCAGATCTCAAAAGAGAGGTCTTCATTACACTGCAGCTTC 780
DB 721 TCCAGGAACTCACTTTACCAGATCTCAAAAGAGAGGTCTTCATTACACTGCAGCTTC 780
QY 781 ATTTTCCAT-----ACATTAAAGATAGTCACT 808
DB 781 ATTTTCCATAGTCACTCAATTTCTGGAGAAATTTCCAGACATTAAGATAGTCACT 840
QY 809 TGGGCTGGTCTGGCGCTGTGTGATGCTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTG 868
DB 841 TGGGCTGGTCTGGCGCTGTGTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 900
QY 869 TGTTCGGTGTGCGAAATGAGAGAGAGGACAGGCTGTGAGGCTTATCTTCACCATCA 928
DB 901 TGTTCGGTGTGCGAAATGAGAGAGAGGACAGGCTGTGAGGCTTATCTTCACCATCA 960
QY 929 TGATTGTTTATTTCTTCTTGGGCTCCCTACAACTTGTCTTCTCTGAAACCTTCC 988
DB 961 TGATTGTTTATTTCTTCTTGGGCTCCCTACAACTTGTCTTCTCTGAAACCTTCC 1020
QY 989 AGGAATCTTTGGCCCTGAATTAATTCAGTAGTCTTAAAGCTTGGACCAAGTATGCAAG 1048
DB 1021 AGGAATCTTTGGCCCTGAATTAATTCAGTAGTCTTAAAGCTTGGACCAAGTATGCAAG 1080
QY 1049 TGACAGAGACTCTTGGGATGAGCAGCTGTGCATCAACCCATCATCTATGCTTTGTCG 1108
DB 1081 TGACAGAGACTCTTGGGATGAGCAGCTGTGCATCAACCCATCATCTATGCTTTGTCG 1140
QY 1109 GGGAGAAGTCTAGAACTACCTCTTGTAGTCTTCTTCCAAAGACATTTGCCAACCTTCT 1168
DB 1141 GGGAGAAGTCTAGAACTACCTCTTGTAGTCTTCTTCCAAAGACATTTGCCAACCTTCT 1200
QY 1169 GCAATCTGTCTTATTTCCAGCAAGAGCTCCGAGGAGCAAGCTCAAGTGGCTTACACC 1228
DB 1201 GCAATCTGTCTTATTTCCAGCAAGAGCTCCGAGGAGCAAGCTCAAGTGGCTTACACC 1260
QY 1229 GATCCACTGGGAGCAGGAAATATCTGTGGGCTTGTGACAGGACTCAAGTGGGCTGGTG 1288
DB 1261 GATCCACTGGGAGCAGGAAATATCTGTGGGCTTGTGACAGGACTCAAGTGGGCTGGTG 1320
QY 1289 ACCGAGTCAAGTGTGCACTGGCTTGTGAGTCTTGTGACAGGACTCAAGTGGGCTGGTG 1348
DB 1321 ACCGAGTCAAGTGTGCACTGGCTTGTGAGTCTTGTGACAGGACTCAAGTGGGCTGGTG 1380
QY 1349 GG---GAGGCTTTTTAAAGGAAGTACTGTTATAGAGGCTTAAAGATTCATCCATTT 1405
DB 1381 TGGNNGAGGCTTTTTAAAGGAAGTACTGTTATAGAGGCTTAAAGATTCATCCATTT 1440
QY 1406 ATTTGGCATCTGTTTAAAGTAGATTAGATCCGAATTC 1442
DB 1441 ATTTGGCATCTGTTTAAAGTAGATTAGATCCGAATTC 1477

RESULT 8
US-09-967-768A-316
; Sequence 316, Application US/09967768A
; Patent No. US2002015087A1
; GENERAL INFORMATION:
; APPLICANT: Augustus, Meena
; TITLE OF INVENTION: Cancer Gene Determination and Therapeutic Screening Using Sign
; FILE OF INVENTION: Sets
; FILE REFERENCE: 689290-72
; CURRENT APPLICATION NUMBER: US/09/967,768A
; CURRENT FILING DATE: 2001-09-28

; PRIOR APPLICATION NUMBER: US/60/236,109
; PRIOR FILING DATE: 2000-09-28
; PRIOR APPLICATION NUMBER: US/60/236,034
; PRIOR FILING DATE: 2000-09-28
; PRIOR APPLICATION NUMBER: US/60/236,111
; PRIOR FILING DATE: 2000-09-28
; NUMBER OF SEQ ID NOS: 325
; SOFTWARE: Patent in version 3.0
; SEQ ID NO 316
; LENGTH: 143068
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-967-768A-316

Query Match 95.4%; Score 1375.2; DB 10; Length 143068;
Best Local Similarity 97.4%; Pred. No. 0;
Matches 1432; Conservative 0; Mismatches 3; Indels 35; Gaps 2;
QY 1 GAATTCCTCCCAACAGCCAAAGCTCTCCATCTAGTGGACAGGAGCTAGCAGCAACCT 60
Db 61244 GAATTCCTCCCAACAGCCAAAGCTCTCCATCTAGTGGACAGGAGCTAGCAGCAACCT 61303
QY 61 TCCTTCACTACAAAACCTTCAATGCTTGGCCAAAAGAGAGATTAATCAATGTAGACATC 120
Db 61304 TCCTTCACTACAAAACCTTCAATGCTTGGCCAAAAGAGAGATTAATCAATGTAGACATC 61363
QY 121 TATGTAGGCAATTAACCACTATTGATGATATAAAGAGTTTGCATTCATGAGGGCAACT 180
Db 61364 TATGTAGGCAATTAACCACTATTGATGATATAAAGAGTTTGCATTCATGAGGGCAACT 61423
QY 181 AATATACATCTAGGACTTTATAAAGATCACTTTTATTTATGACAGGGTGAACAAGA 240
Db 61424 AATATACATCTAGGACTTTATAAAGATCACTTTTATTTATGACAGGGTGAACAAGA 61483
QY 241 TGGATTATCAAGTGTCAAGTCCAAATCTATGACATCAATTAATATACATCGGAGCCCTGCC 300
Db 61484 TGGATTATCAAGTGTCAAGTCCAAATCTATGACATCAATTAATATACATCGGAGCCCTGCC 61543
QY 301 AAAAATCAATGTCAAGCAATTCGACCGCCCTCTGCTCCCTCCGCTACCTACCTGCTGT 360
Db 61544 AAAAATCAATGTCAAGCAATTCGACCGCCCTCTGCTCCCTCCGCTACCTACCTGCTGT 61603
QY 361 TCATCTTTGGTTTGTGGGCAACATGCTGTCTCATCTCTCATCTGATATAAATGCAAAAGGC 420
Db 61604 TCATCTTTGGTTTGTGGGCAACATGCTGTCTCATCTCTCATCTGATATAAATGCAAAAGGC 61663
QY 421 TGAAGAGATGACATGACATCTACCTGCTCAACCTGGCCATCTGACCTGTTTTCCTTC 480
Db 61664 TGAAGAGATGACATGACATCTACCTGCTCAACCTGGCCATCTGACCTGTTTTCCTTC 61723
QY 481 TTACTGTCCTCCCTCTGGGCTCACTATGCTGCGCCAGTGGGACCTTTGGAATACAAATGT 540
Db 61724 TTACTGTCCTCCCTCTGGGCTCACTATGCTGCGCCAGTGGGACCTTTGGAATACAAATGT 61783
QY 541 GTCAACTCTTGACAGGCTCTATTTATAGGCTTCTCTCTGGAATCTTCTTCATCATCC 600
Db 61784 GTCAACTCTTGACAGGCTCTATTTATAGGCTTCTCTCTGGAATCTTCTTCATCATCC 61843
QY 601 TCTGTACATCGATAGTACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 660
Db 61844 TCTGTACATCGATAGTACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 61903
QY 661 CGGTACCTTTGGGCTGGTGACAAAGTGTGATCACTTGGGTGGGTGCTGCTGCTGCTGCTGCT 720
Db 61904 CGGTACCTTTGGGCTGGTGACAAAGTGTGATCACTTGGGTGGGTGCTGCTGCTGCTGCTGCT 61963
QY 721 TCCAGGATCATCTTTACAGATCTCAAAAGAGTCTTCATTCACCTGCACTGCTC 780
Db 61964 TCCAGGATCATCTTTACAGATCTCAAAAGAGTCTTCATTCACCTGCACTGCTC 62023
QY 781 ATTTTCCAT-----ACATTAAGATAGTCACT 808
Db 62024 ATTTTCCATAGCTAGTATCAATTCGGAAGAAATTTCCAGACATTAAGATAGTCACT 62083

QY 809 TGGGGCTGGTCTCGCCGCTGCTGTGTCATGTCATCTGCTACTCGGAATCTCTAAAACTC 868
Db 62084 TGGGGCTGGTCTCGCCGCTGCTGTGTCATGTCATCTGCTACTCGGAATCTCTAAAACTC 62143
QY 869 TGCCTCGGCTGCAATGAG 928
Db 62144 TGCCTCGGCTGCAATGAG 62203
QY 929 TGATTTGTTTATTTTCTCTTCTGGGCTCCCTCAACATTTGCTTCTCTCTCTCTCTCTCTCT 988
Db 62204 TGATTTGTTTATTTTCTCTCTGGGCTCCCTCAACATTTGCTTCTCTCTCTCTCTCTCTCT 62263
QY 989 AGGAATCTTTGGCCTGAATTAATGTCAGTGTCTTAACAGGTTGGACCAAGCTATGCAAG 1048
Db 62264 AGGAATCTTTGGCCTGAATTAATGTCAGTGTCTTAACAGGTTGGACCAAGCTATGCAAG 62323
QY 1049 TGACAGAGACTCTTGGGATGACGACTGCTGTCATCAACCCCATCATCTATGCTTTGTGG 1108
Db 62324 TGACAGAGACTCTTGGGATGACGACTGCTGTCATCAACCCCATCATCTATGCTTTGTGG 62383
QY 1109 GGGAGAAGTTTCAAGAACTTACCTCTTCTTCTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT 1168
Db 62384 GGGAGAAGTTTCAAGAACTTACCTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 62443
QY 1169 GCAATGCTGTTCTATTTTCCAGAAAGAGGCTCCCGAGCGAGCAAGCTCAGTTTACACCC 1228
Db 62444 GCAATGCTGTTCTATTTTCCAGAAAGAGGCTCCCGAGCGAGCAAGCTCAGTTTACACCC 62503
QY 1229 GATCCACTGGGAGCAGCAAAATATCTGTGGCTTGTGACACGACTCAGTGGGCTGGTG 1288
Db 62504 GATCCACTGGGAGCAGCAAAATATCTGTGGCTTGTGACACGACTCAGTGGGCTGGTG 62563
QY 1289 ACCAGTCAAGTGTGACATGCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 1346
Db 62564 ACCAGTCAAGTGTGACATGCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 62623
QY 1347 -TTGGGAGGCTCTTTTAAAGAGAGTACTGTTATAGAGGGTCTAAGATTTCATCCATTT 1405
Db 62624 TGGGAGAGGCTCTTTTAAAGAGAGTACTGTTATAGAGGGTCTAAGATTTCATCCATTT 62683
QY 1406 ATTTGGCATCTGTTTAAAGTAGATTAGATC 1435
Db 62684 ATTTGGCATCTGTTTAAAGTAGATTAGATC 62713

RESULT 9
US-10-086-814-2
; Sequence 2, Application US/10086814
; Publication No. US20030092632A1
; GENERAL INFORMATION:
; APPLICANT: Dragic, Tatjana
; APPLICANT: Olson, William C.
; TITLE OF INVENTION: SULFATED CCR5 PEPTIDES FOR HIV-1 INFECTION
; FILE REFERENCE: 61010-AB-1
; CURRENT APPLICATION NUMBER: US/10/086,814
; CURRENT FILING DATE: 2002-02-28
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 2
; LENGTH: 1376
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-086-814-2

Query Match 90.3%; Score 1302; DB 9; Length 1376;
Best Local Similarity 97.7%; Pred. No. 0;
Matches 1344; Conservative 0; Mismatches 0; Indels 32; Gaps 1;
QY 1 GAATTCCTCCCAACAGCCAAAGCTCTCCATCTAGTGGACAGGAGCTAGCAGCAACCT 60
Db 1 GAATTCCTCCCAACAGCCAAAGCTCTCCATCTAGTGGACAGGAGCTAGCAGCAACCT 60

QY 61 TCCCTTCACTACAAAGCTTCATTGCTTGGCCAAAAGAGAGTTAATTCAATGTAGACATC 120
Db 61 TCCCTTCACTACAAAGCTTCATTGCTTGGCCAAAAGAGAGTTAATTCAATGTAGACATC 120
QY 121 TATGTAGGCAATTAATAACCTATTGATGTATAAACAAGTTTGCAATTCATGAGGGCAACT 180
Db 121 TATGTAGGCAATTAATAACCTATTGATGTATAAACAAGTTTGCAATTCATGAGGGCAACT 180
QY 181 AAATACATCTTACGAGCTTTATAAAGATCATTCTTTTATATGACAGGGTGAACAAGA 240
Db 181 AAATACATCTTACGAGCTTTATAAAGATCATTCTTTTATATGACAGGGTGAACAAGA 240
QY 241 TGGATATCAAGTGTCAAGTCCATCTATGACATCAATTTATATACATCGAGCCCTGCC 300
Db 241 TGGATATCAAGTGTCAAGTCCATCTATGACATCAATTTATATACATCGAGCCCTGCC 300
QY 301 AAAAATCAATGTGAAGCAATCGAGCCCGCTCCCTCGCTCTACTCACTGGTGT 360
Db 301 AAAAATCAATGTGAAGCAATCGAGCCCGCTCCCTCGCTCTACTCACTGGTGT 360
QY 361 TCATCTTTGTTTGTGGCAACATGCTGCTCATCTCTCATCTGATTAACHTGGAAGGC 420
Db 361 TCATCTTTGTTTGTGGCAACATGCTGCTCATCTCTCATCTGATTAACHTGGAAGGC 420
QY 421 TGAAGAGCATGACTGACATCTACCTGCTCAACCTGGCCATCTCTGACCTGTTTTCTTC 480
Db 421 TGAAGAGCATGACTGACATCTACCTGCTCAACCTGGCCATCTCTGACCTGTTTTCTTC 480
QY 481 TTACTGTCCCTTCGGCTCAGTATGCTGCGGCCAGTGGGACTTTGGAATCAATGT 540
Db 481 TTACTGTCCCTTCGGCTCAGTATGCTGCGGCCAGTGGGACTTTGGAATCAATGT 540
QY 541 GTCAACTCTGTGAGGGCTCTATTATATAGGCTCTCTCTGGAATCTCTTCATCATCC 600
Db 541 GTCAACTCTGTGAGGGCTCTATTATATAGGCTCTCTCTGGAATCTCTTCATCATCC 600
QY 601 TCCGTGCAATFCGATAGTACCTGGCTGCTGCTCATCTGCTGTTGTTGTTAAAGCCAGGA 660
Db 601 TCCGTGCAATFCGATAGTACCTGGCTGCTGCTCATCTGCTGTTGTTGTTAAAGCCAGGA 660
QY 661 CGGTACCTTTGGGCTGTGACAGTGTGATCATTGGTGGTGGCTGTTGCTGCTC 720
Db 661 CGGTACCTTTGGGCTGTGACAGTGTGATCATTGGTGGTGGCTGTTGCTGCTC 720
QY 721 TCCAGGAATCATCTTTACAGATCTCAAAAAGAGTCTTCAATACACTGCAAGCTC 780
Db 721 TCCAGGAATCATCTTTACAGATCTCAAAAAGAGTCTTCAATACACTGCAAGCTC 780
QY 781 ATTTTCCAT-----ACATTAAGATAGTCACT 808
Db 781 ATTTTCCATACAGTCACTATCAATTTCTGGAAGATTTCCAGACATTTAAAGATAGTCACT 840
QY 809 TGGGCTGGTCCCTGCGCTGTTGCTATGCTCATCTGCTACTCGGGAATCTTAAACATC 868
Db 841 TGGGCTGGTCCCTGCGCTGTTGCTATGCTCATCTGCTACTCGGGAATCTTAAACATC 900
QY 869 TCGTTCGGTTCGAATGAGAAGAGGACACAGGCTGTGAGGCTTATCTTCACCATCA 928
Db 901 TCGTTCGGTTCGAATGAGAAGAGGACACAGGCTGTGAGGCTTATCTTCACCATCA 960
QY 929 TGATGTTTATTTCTCTTCCTGGGCTCCCTACACATGTCCTTCCTGAAACACCTTC 988
Db 961 TGATGTTTATTTCTCTTCCTGGGCTCCCTACACATGTCCTTCCTGAAACACCTTC 1020
QY 989 AGGAATCTTTGGCTGGAATTAATGCAAGTCTTAACAGTTGGACACAGTATGAGG 1048
Db 1021 AGGAATCTTTGGCTGGAATTAATGCAAGTCTTAACAGTTGGACACAGTATGAGG 1080
QY 1049 TGACAGAGACTCTTGGGATGAGCAGTGTGCTATCAACCCCATCTATGCTGCTTGTG 1108
Db 1081 TGACAGAGACTCTTGGGATGAGCAGTGTGCTATCAACCCCATCTATGCTGCTTGTG 1140
QY 1109 GGGAGAGTTTCAGAACTAOCCTTCTTCTTCTTCCAAAAGCACATTCGCAAGCTTCT 1168

Db 1141 GGGAGAGTTTCAGAACTAOCCTTCTTCTTCTTCCAAAAGCACATTCGCAAGCTTCT 1200
QY 1169 GCAATGCTGTTCTATTCTTCCAGCAAGAGGCTCCCGAGCGAGCAAGCTCAGTTTACACCC 1228
Db 1201 GCAATGCTGTTCTATTCTTCCAGCAAGAGGCTCCCGAGCGAGCAAGCTCAGTTTACACCC 1260
QY 1229 GATCCTATGGGGAGCAGGAATAATCTCTGTTGGCTTGTGACAGGACTCAAGTGGGCTGGTG 1288
Db 1261 GATCCTATGGGGAGCAGGAATAATCTCTGTTGGCTTGTGACAGGACTCAAGTGGGCTGGTG 1320
QY 1289 ACCAGTCAAGTGTGACATGCTTAGTTTTCATACACAGCTGGGCTGGGCTG 1344
Db 1321 ACCAGTCAAGTGTGACATGCTTAGTTTTCATACACAGCTGGGCTGGGCTG 1376

RESULT 10
US-09-796-202-2
; Sequence 2, Application US/09796202
; Patent No. US20020068813A1
; GENERAL INFORMATION:
; APPLICANT: Dragic, Tatjana
; APPLICANT: Olson, William
; FILE OF INVENTION: SULFATED CCR5 PEPTIDES FOR HIV-1 INFECTION
; FILE REFERENCE: 2048/61010/JPM/SHS
; CURRENT APPLICATION NUMBER: US/09/796,202
; CURRENT FILING DATE: 2001-02-28
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2
; LENGTH: 1376
; TYPE: DNA
; ORGANISM: human
US-09-796-202-2

Query Match 90.3%; Score 1302; DB 10; Length 1376;
Best Local Similarity 97.7%; Pred. No. 0;
Matches 1344; Conservative 0; Mismatches 0; Indels 32; Gaps 1;

QY 1 GAATTCCTCCCAACAGAGCCAGCTCTCCATCTAGTGGCAGGGAAGCTAGCAGCAAACT 50
Db 1 GAATTCCTCCCAACAGAGCCAGCTCTCCATCTAGTGGCAGGGAAGCTAGCAGCAAACT 60
QY 61 TCCCTTCACTACAAACTTCATTGCTTGGCCAAAAGAGAGTTAATTCAATGTAGACATC 120
Db 61 TCCCTTCACTACAAACTTCATTGCTTGGCCAAAAGAGAGTTAATTCAATGTAGACATC 120
QY 121 TATGTAGGCAATTAATAACCTATTGATGTATAAACAAGTTTGCAATTCATGAGGGCAACT 180
Db 121 TATGTAGGCAATTAATAACCTATTGATGTATAAACAAGTTTGCAATTCATGAGGGCAACT 180
QY 181 AAATACATCTGAGACTTTATAAAGATCACTTTTATATGACAGGGTGAACAAGA 240
Db 181 AAATACATCTGAGACTTTATAAAGATCACTTTTATATGACAGGGTGAACAAGA 240
QY 241 TGGATATCAAGTGTCAAGTCCATCTATGACATCAATTTATATACATCGAGCCCTGCC 300
Db 241 TGGATATCAAGTGTCAAGTCCATCTATGACATCAATTTATATACATCGAGCCCTGCC 300
QY 301 AAAAATCAATGTGAAGCAATCGAGCCCGCTCCCTCGCTCTACTCACTGGTGT 360
Db 301 AAAAATCAATGTGAAGCAATCGAGCCCGCTCCCTCGCTCTACTCACTGGTGT 360
QY 361 TCATCTTTGTTTGTGGCAACATGCTGCTCATCTCTCATCTGATTAACHTGGAAGGC 420
Db 361 TCATCTTTGTTTGTGGCAACATGCTGCTCATCTCTCATCTGATTAACHTGGAAGGC 420
QY 421 TGAAGAGCATGACTGACATCTACCTGCTCAACCTGGCCATCTCTGACCTGTTTTCTTC 480
Db 421 TGAAGAGCATGACTGACATCTACCTGCTCAACCTGGCCATCTCTGACCTGTTTTCTTC 480
QY 481 TTACTGTCCCTTCGGCTCAGTATGCTGCGGCCAGTGGGACTTTGGAATCAATGT 540

Db 481 TTACTGTCCTCCCTCTGGGCTCAGTATGCTGCCGCCAGTGGGACTTTGGAAATACATCT 540
QY 541 GTCAACTCTGTGACAGGCTCTATTTATATAGGCTTCTCTGGAATCTTCTTCATCATCC 600
Db 541 GTCAACTCTGTGACAGGCTCTATTTATATAGGCTTCTCTGGAATCTTCTTCATCATCC 600
QY 601 TCTGTACATCGATAGTACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 560
Db 601 TCTGTACATCGATAGTACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 560
QY 661 CGGTCACTTTGGGCTGGTGCACAGTGTGATCAGTGTGGTGGTGGTGGTGGTGGTGGT 720
Db 661 CGGTCACTTTGGGCTGGTGCACAGTGTGATCAGTGTGGTGGTGGTGGTGGTGGTGGT 720
QY 721 TCCAGGAATCATTTTACAGATCTCAAAAGAGTGTTCATTTACACCTGCGAGTCTC 780
Db 721 TCCAGGAATCATTTTACAGATCTCAAAAGAGTGTTCATTTACACCTGCGAGTCTC 780
QY 781 ATTTTCCAT-----ACATTAAGATAGTCACT 808
Db 781 ATTTTCCATPACAGTCACTATCAATCTGGAAGAAATTTCCAGACATTTAAAGATAGTCACT 840
QY 809 TGGGGCTGGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 868
Db 841 TGGGGCTGGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 900
QY 869 TGGTTCGGTGTGGAATGAGAAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 928
Db 901 TGGTTCGGTGTGGAATGAGAAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 960
QY 929 TGATTTGTTATTTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 988
Db 961 TGATTTGTTATTTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1020
QY 989 AGGANTCTTTGGGCTGGAATTAATGAGTACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1048
Db 1021 AGGANTCTTTGGGCTGGAATTAATGAGTACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1080
QY 1049 TGACAGAGACTTTGGGAGTGGGAGTGGGAGTGGGAGTGGGAGTGGGAGTGGGAGTGGGAG 1108
Db 1081 TGACAGAGACTTTGGGAGTGGGAGTGGGAGTGGGAGTGGGAGTGGGAGTGGGAGTGGGAG 1140
QY 1109 GGGAGAGTTCAGAACTACTCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1168
Db 1141 GGGAGAGTTCAGAACTACTCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1200
QY 1169 GCAATGCTGCTTCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1228
Db 1201 GCAATGCTGCTTCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1260
QY 1229 GATCCACTGGGAGCAGGAATATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1288
Db 1261 GATCCACTGGGAGCAGGAATATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1320
QY 1289 ACCGATCAGAGTGTGCAATGGCTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1344
Db 1321 ACCGATCAGAGTGTGCAATGGCTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1376

RESULT 11

US-10-232-686-1
; Sequence 1, Application US/10232686
; Publication No. US20030023044A1
; GENERAL INFORMATION:
; APPLICANT: Li, Yi
; APPLICANT: Ruben, Steven M.
; TITLE OF INVENTION: Human G-Protein Chemokine Receptor (CCR5) HDGNR10
; FILE REFERENCE: 1488.115000N
; CURRENT APPLICATION NUMBER: US/10/232,686
; CURRENT FILING DATE: 2002-09-03
; PRIOR APPLICATION NUMBER: 09/339,912
; PRIOR FILING DATE: 1999-06-25
; PRIOR APPLICATION NUMBER: 09/195,662

; PRIOR FILING DATE: 1998-11-18
; PRIOR APPLICATION NUMBER: 08/466,343
; PRIOR FILING DATE: 1995-06-06
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1
; LENGTH: 1414
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (259)..(1314)
US-10-232-686-1

Query Match 89.7%; Score 1293.4; DB 9; Length 1414;
Best Local Similarity 96.6%; Pred. No. 0;
Matches 1345; Conservative 0; Mismatches 16; Indels 32; Gaps 1;

QY 2 AATTCCTCCCAACAGAGCAAGCTCTCCATCTAGTGGCAGGAGAGCTAGCAGCAAACTT 61
Db 21 AATTCCTCCCAACAGAGCAAGCTCTCCATCTAGTGGCAGGAGAGCTAGCAGCAAACTT 80
QY 62 CCCTTCTACTACAAACTTTCATTTGCTGGCCAAAAGAGAGTAAATTCATGTAGCAATCT 121
Db 81 CCCTTCTACTACAAACTTTCATTTGCTGGCCAAAAGAGAGTAAATTCATGTAGCAATCT 140
QY 122 ATGTAGCAATTAATAAACCCTATTGATGATATAAAACAGTTTGCAATTCATGGAGGCAACTA 181
Db 141 ATGTAGCAATTAATAAACCCTATTGATGATATAAAACAGTTTGCAATTCATGGAGGCAACTA 200
QY 182 AATACATCTAGAGCTTTTATAAAGATCACTTTTATATATGACAGGTTGGAACAAGAT 241
Db 201 AATACATCTAGAGCTTTTATAAAGATCACTTTTATATATGACAGGTTGGAACAAGAT 260
QY 242 GGATTAATCAAGTGTCAAGTCCCAATCTATGACATCAATTAATATATACATGGAGCCCTGCCA 301
Db 261 GGATTAATCAAGTGTCAAGTCCCAATCTATGACATCAATTAATATATACATGGAGCCCTGCCA 320
QY 302 AAAAATCAATGTGAAGAAATTCGACAGCCGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 361
Db 321 AAAAATCAATGTGAAGAAATTCGACAGCCGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 380
QY 362 CATCTTTGGTGTGTTGGCAGCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 421
Db 381 CATCTTTGGTGTGTTGGCAGCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 440
QY 422 GAAGAGCATGACATGACATCTACCTGCTCAACCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 481
Db 441 GAAGAGCATGACATGACATCTACCTGCTCAACCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 500
QY 482 TACTGTCCCTTCTGGGCTCACTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 541
Db 501 TACTGTCCCTTCTGGGCTCACTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 560
QY 542 TCAACTCTTGCACAGGCTCTATTTTATAGGCTTCTCTGCTGCTGCTGCTGCTGCTGCTGCT 601
Db 561 TCAACTCTTGCACAGGCTCTATTTTATAGGCTTCTCTGCTGCTGCTGCTGCTGCTGCTGCT 620
QY 602 COTGCAATCGATAGGTACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 661
Db 621 COTGCAATCGATAGGTACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 680
QY 662 GGTCACTTTGGGTTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGT 721
Db 681 GGTCACTTTGGGTTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGT 740
QY 722 CCCAGGAATCACTTTTACAGATCTCAAAAGAGGCTTCTTATACCTGCTGCTGCTGCTGCTGCT 781
Db 741 CCCAGGAATCACTTTTACAGATCTCAAAAGAGGCTTCTTATACCTGCTGCTGCTGCTGCTGCT 800
QY 782 TTTTCCAT-----ACATTAAGATAGTCACTTT 809
Db 801 TTTTCCATACAGTCACTATCAATTTCTGGAAGAAATTTCCAGACATTAAGATAGTCACTTT 860

Db 1341 CCCACTCAGATTGTCACATGGCTTAGTTTTCATACACAGCCTGGGCTGGGGTGGGGT 1400
QY 1350 GGAGGCTTTTTT 1362
Db 1401 GGAAGAGTCTTT 1413

RESULT 14
US-09-339-912A-1
; Sequence 1, Application US/09339912A
; Patent No. US20020099176A1
; GENERAL INFORMATION:
; APPLICANT: Li, Yi
; APPLICANT: Ruben, Steven M.
; TITLE OF INVENTION: Antibodies to Human G-Protein Chemokine Receptor HDGNR10
; FILE OF INVENTION: (CCRS Receptor)
; FILE REFERENCE: 1488.1150003
; CURRENT APPLICATION NUMBER: US/09/339,912A
; PRIOR FILING DATE: 1999-06-25
; PRIOR APPLICATION NUMBER: 09/195,662
; PRIOR FILING DATE: 1998-11-18
; PRIOR APPLICATION NUMBER: 08/466,343
; PRIOR FILING DATE: 1995-06-06
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1
; LENGTH: 1414
; TYPE: DNA
; ORGANISM: Artificial Sequence: Genomic
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (259)..(1314)
; OTHER INFORMATION: Description of Artificial Sequence: Genomic
US-09-339-912A-1

Query Match 89.7%; Score 1293.4; DB 10; Length 1414;
Best Local Similarity 96.6%; Pred. No. 0;
Matches 1345; Conservative 0; Mismatches 16; Indels 32; Gaps 1;

QY 2 AATTCGCCCAACAGCCAGCTCTCCATCTAGTCAGCAGGAGCTAGCAGCAACCTT 61
Db 21 ATTCGCCCAACAGCCAGCTCTCCATCTAGTCAGCAGGAGCTAGCAGCAACCTT 80
QY 62 CCTCTCACTCAAACTTCATGTCTGGCCAAAAGAGAGTTAATCAATGTAGACACT 121
Db 81 CCTCTCACTCAAACTTCATGTCTGGCCAAAAGAGAGTTAATCAATGTAGACACT 140
QY 122 ATGTAGGCAATTAACCACTTATGATGTATTAACAGTTTGCATTCATGGAGGCACTA 161
Db 141 ATGTAGGCAATTAACCACTTATGATGTATTAACAGTTTGCATTCATGGAGGCACTA 200
QY 182 AATCACTCTAGGACATTAATAAGATCACTTTTATTTATGACAGGCTGGAACAAGAT 241
Db 201 AATCACTCTAGGACATTAATAAGATCACTTTTATTTATGACAGGCTGGAACAAGAT 260
QY 242 GAATATCAAGTGTCAAGTCCAACTATGACATCAATTAATATACATCGGAGCCCTGCCA 301
Db 261 GAATATCAAGTGTCAAGTCCAACTATGACATCAATTAATATACATCGGAGCCCTGCCA 320
QY 302 AAAATCAATGCAAGCAATCGCAGCCGCTCTGCTCCGCTCTACTCTACTGGTGT 361
Db 321 AAAATCAATGCAAGCAATCGCAGCCGCTCTGCTCCGCTCTACTCTACTGGTGT 380
QY 362 CATCTTTGGTTTGTGGGCAACATCGTGTCTCATCTCTGATATAAATCGCAAAAGCT 421
Db 381 CATCTTTGGTTTGTGGGCAACATCGTGTCTCATCTCTGATATAAATCGCAAAAGCT 440
QY 422 GAAGACATGACTGACATCTACCTGCTCAACTGGCCATCTCTGACCTGTTTTCCTCT 481
Db 441 GAAGACATGACTGACATCTACCTGCTCAACTGGCCATCTCTGACCTGTTTTCCTCT 500
QY 482 TACTCTCCCTCTCTGGCTCTACTATGCTGCGCCGCTGAGCTTTGGAATACAAATGTG 541

Db 501 TACTGTCCCTCTCTGGCTCACTATGCTGCCGCCAGTGGGACTTTGAAATACATATGTG 560
QY 542 TCAACTCTTTGACAGGCTCTATTTTATAGGCTTCTCTCTGCAATCTCTCTCATCATCTT 601
Db 561 TCAACTCTTTGACAGGCTCTATTTTATAGGCTTCTCTCTGCAATCTCTCTCATCATCTT 620
QY 602 CTGCAATCGATAGTACCTGCTGCTGCTCCATGCTGTGTTTGTCTTTAAAGCCAGGAC 661
Db 621 CTGCAATCGATAGTACCTGCTGCTGCTCCATGCTGTGTTTGTCTTTAAAGCCAGGAC 680
QY 662 GPTCACTTTGGGCTGTGACAAAGTGTGATCACTTGGGTGGTGGCTGTGTTTCCGTCTCT 721
Db 681 GPTCACTTTGGGCTGTGACAAAGTGTGATCACTTGGGTGGTGGCTGTGTTTCCGTCTCT 740
QY 722 CCAGGAATCATCTTTTACCAGATCTCAAAAGAGAGCTTTCATTACACCTGAGCTCTCA 781
Db 741 CCAGGAATCATCTTTTACCAGATCTCAAAAGAGAGCTTTCATTACACCTGAGCTCTCA 800
QY 782 TTTTCCAT-----ACATTAAGATAGTCACTT 809
Db 801 TTTTCCATAGTCACTATCAATTTCCAGAAATTTCCAGACATTAAGATAGTCACTT 860
QY 810 GGGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 869
Db 861 GGGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 920
QY 870 GCTTGGTGTGAAATGAGAAGAGGACACAGGCTGTGAGGCTTATCTTCCACCATCAT 929
Db 921 GCTTGGTGTGAAATGAGAAGAGGACACAGGCTGTGAGGCTTATCTTCCACCATCAT 980
QY 930 GATTGTTTATTTCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 989
Db 981 GATTGTTTATTTCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1040
QY 990 GGAATCTTTGGCTGAAATTAATTCAGTGTAGTCTTAACAGGTTGGACCAAGCTATGAGGT 1049
Db 1041 GGAATCTTTGGCTGAAATTAATTCAGTGTAGTCTTAACAGGTTGGACCAAGCTATGAGGT 1100
QY 1050 GACAGAGACTCTTGGGATGAGGACTGTGCTATCAACCCCATCACTATGCTTTGCTGG 1109
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Db 1161 GGAAGAGTTGAGAACTTACCTCTTCTCTCTTCCAAAAGACATTCGCAAGCTCTTG 1220
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QY 1230 ATCCACTGGGAGCAGGAATATCTTGGGCTGTGACACGAGCTCAAGTGGGCTGGTGA 1289
Db 1281 ATCCACTGGGAGCAGGAATATCTTGGGCTGTGACACGAGCTCAAGTGGGCTGGTGA 1340
QY 1290 CCAAGTCAAGTGTGACATGCTTGTATTTTATACACAGCTGGGCTGGGCTGGGCTGG 1349
Db 1341 CCAAGTCAAGTGTGACATGCTTGTATTTTATACACAGCTGGGCTGGGCTGGGCTGG 1400
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Db 1401 GGAAGAGTCTTT 1413

RESULT 15

US-09-502-783A-1

; Sequence 1, Application US/09502783A

; Patent No. US20020132269A1

; GENERAL INFORMATION:

; APPLICANT: Li, Yi

; APPLICANT: Ruben, Steven M.

; TITLE OF INVENTION: Polynucleotides Encoding Human G-Protein Chemokine Receptor (C

; TITLE OF INVENTION: HDGNR10

; FILE REFERENCE: 1488.1150006

; CURRENT APPLICATION NUMBER: US/09/502,783A
 ; CURRENT FILING DATE: 2001-08-23
 ; PRIOR APPLICATION NUMBER: 08/466,343
 ; PRIOR FILING DATE: 1995-06-06
 ; NUMBER OF SEQ ID NOS: 9
 ; SOFTWARE: PatentIn version 3.0
 ; SEQ ID NO 1
 ; LENGTH: 1414
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 ; FEATURE:
 ; NAME/KEY: CDS
 ; LOCATION: (259)..(1314)
 ; US-09-502-783A-1

Query Match 89.7%; Score 1293.4; DB 10; Length 1414;
 Best Local Similarity 96.6%; Pred. No. 0;
 Matches 1345; Conservative 0; Mismatches 16; Indels 32; Gaps 1;

QY	2	AATCCCCCAACAGCCAGCTCCATCTAGTGGACAGGAGCTAGCAGCAACCTT	51
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QY	62	CCCTTCACATACAAACTCATCTGCTGGCCAAAGAGAGTTAAATCAATGACATCT	121
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QY	122	ATGAGGCAATTAACACCTATTGATGATATAACAGTTGCAATGAGGAGGCAACTA	181
DB	141	ATGAGGCAATTAACACCTATTGATGATATAACAGTTGCAATGAGGAGGCAACTA	200
QY	182	AATACATCTAGGACTTTATAAAGATCACCTTTTATATGACAGGGTGGACAAAGAT	241
DB	201	AATACATCTAGGACTTTATAAAGATCACCTTTTATATGACAGGGTGGACAAAGAT	260
QY	242	GGATTAATCAAGTCAAGTCCCAATCATGACATCAATTAATATATACATCGGAGCCGCA	301
DB	261	GGATTAATCAAGTCAAGTCCCAATCATGACATCAATTAATATATACATCGGAGCCGCA	320
QY	302	AAAAATCAATGTGAAGCAAAATGCGAGCCGCTCTGCTCGCTGCTACTACTCTGTTGT	361
DB	321	AAAAATCAATGTGAAGCAAAATGCGAGCCGCTCTGCTCGCTGCTACTACTCTGTTGT	380
QY	362	CATCTTTGGTTTTGTGGCAACATGCTGCTCATCTCATCTGATAAAGCTGCAAAAGCTT	421
DB	381	CATCTTTGGTTTTGTGGCAACATGCTGCTCATCTCATCTGATAAAGCTGCAAAAGCTT	440
QY	422	GAAGACATGATGACATCTACCTGCTCAACCTGGCCATCTGACCTGTTTTCTCTCT	481
DB	441	GAAGACATGATGACATCTACCTGCTCAACCTGGCCATCTGACCTGTTTTCTCTCT	500
QY	482	TACTGTCCTCTTGGGCTCAGTATGCTGCTGCGCCGCTGAGCTTTGGAATACAATGTG	541
DB	501	TACTGTCCTCTTGGGCTCAGTATGCTGCTGCGCCGCTGAGCTTTGGAATACAATGTG	560
QY	542	TCACATCTTGAAGGCTCTATTTATAGGCTTCTCTCTGGAATCTTCTTCATCATCT	601
DB	561	TCACATCTTGAAGGCTCTATTTATAGGCTTCTCTCTGGAATCTTCTTCATCATCT	620
QY	602	CCCTGCAATTCGATAGTACCTGCTGCTGCTGCTGCTGCTTTTAAAGCCAGGAC	661
DB	621	CCCTGCAATTCGATAGTACCTGCTGCTGCTGCTGCTGCTTTTAAAGCCAGGAC	680
QY	662	GGTCACCTTTGGGTTGGTGAAGTGTGATCAGTTGGTGGTGGTGGTGGTGGTGGTGGT	721
DB	681	GGTCACCTTTGGGTTGGTGAAGTGTGATCAGTTGGTGGTGGTGGTGGTGGTGGTGGT	740
QY	722	CCCAGGAATCATCTTTACAGATCTCAAAAGAGGCTCTTCAATACACCTGCAGCTCTCA	781
DB	741	CCCAGGAATCATCTTTACAGATCTCAAAAGAGGCTCTTCAATACACCTGCAGCTCTCA	800
QY	782	TTTTCCAT-----ACATTAAGATAGTCAATCTT	809

DB	801	TTTTCCATCAGTCAGTATCAATCTTGGAGAAATTCACAGACATTAAAGATGATCATCTT	860
QY	810	GGGGCTGGTCTCGCGCTGTGTGTCATGTCATCTGCGGAAATCCTTAAAGATCT	869
DB	861	GGGGCTGGTCTCGCGCTGTGTGTCATGTCATCTGCGGAAATCCTTAAAGATCT	920
QY	870	CGTTCCGCTGTCGAATGAGAAAGAGGACAGGCGCTGTGAGGCTTATCTTCACCATCAT	929
DB	921	CGTTCCGCTGTCGAATGAGAAAGAGGACAGGCGCTGTGAGGCTTATCTTCACCATCAT	980
QY	930	GATTGTTTATTTCTCTTGGGCTCCCTACAAACATTTCTCTCTCTCTCTCTCTCTCTCT	989
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QY	990	GGAAATCTTTGGCGCTGAATAATTCAGTAGCTCTTAACAGTTTGGACCAAGCTATGAGGT	1049
DB	1041	GGAAATCTTTGGCGCTGAATAATTCAGTAGCTCTTAACAGTTTGGACCAAGCTATGAGGT	1100
QY	1050	GACAGACATCTTTGGGATGACGCACTGCTGCATCAACCCCATCATCTATGCTTGTGCG	1109
DB	1101	GACAGACATCTTTGGGATGACGCACTGCTGCATCAACCCCATCATCTATGCTTGTGCG	1160
QY	1110	GGAGAAGTTTCAGAAACTACCTCTTTAGTCTCTTCCAAAGACATTCGCAACGCTCTG	1169
DB	1161	GGAGAAGTTTCAGAAACTACCTCTTTAGTCTCTTCCAAAGACATTCGCAACGCTCTG	1220
QY	1170	CAATGCTGTTCTATTTTCCAGGAGAGGCTCCCGAGGAGCAAGCTCAGTTTACACCG	1229
DB	1221	CAATGCTGTTCTATTTTCCAGGAGAGGCTCCCGAGGAGCAAGCTCAGTTTACACCG	1280
QY	1230	ATCCACTGGGGAGCAGGAAATATCTGTGGGCTTGTGACAGGACTCAAGTGGGCTGGA	1289
DB	1281	ATCCACTGGGGAGCAGGAAATATCTGTGGGCTTGTGACAGGACTCAAGTGGGCTGGA	1340
QY	1290	CCCACTCAGAGTTGTGCAATGGCTTAGTTTATACACAGCCCTGGGCTGGGCTGGGCTG	1349
DB	1341	CCCACTCAGAGTTGTGCAATGGCTTAGTTTATACACAGCCCTGGGCTGGGCTGGGCTG	1400
QY	1350	GGAGGCTCTTTT 1362	
DB	1401	GGAGAGGCTCTTT 1413	

Search completed: June 8, 2003, 10:50:57
 Job time : 228 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: June 8, 2003, 06:22:47 ; Search time 2337 Seconds
(without alignments)
10439.827 Million cell updates/sec

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Perfect score: 1442
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Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 16154066 seqs, 8097743376 residues
Total number of hits satisfying chosen parameters: 32308132

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : EST.*

- 1: em_estba.*
- 2: em_esthum.*
- 3: em_estin.*
- 4: em_estm.*
- 5: em_estov.*
- 6: em_estpi.*
- 7: em_estro.*
- 8: em_hic.*
- 9: gb_est1.*
- 10: gb_est2.*
- 11: gb_hic.*
- 12: gb_est3.*
- 13: gb_est4.*
- 14: gb_est5.*
- 15: em_estfun.*
- 16: em_estom.*
- 17: gb_gss.*
- 18: em_gss_hum.*
- 19: em_gss_inv.*
- 20: em_gss_pln.*
- 21: em_gss_vrt.*
- 22: em_gss_fun.*
- 23: em_gss_man.*
- 24: em_gss_mus.*
- 25: em_gss_other.*
- 26: em_gss_pro.*
- 27: em_gss_rod.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	654	45.4	807	13	BI764263
2	360.6	25.0	487	10	BE656336
3	327.8	22.7	542	9	AA547303
4	322	22.3	452	9	AI851510
5	315.6	21.9	480	10	AW657263
6	280.8	19.5	447	9	AA671573

7	272.2	18.9	907	9	AL552677
8	268	18.6	1074	14	BM917063
9	222.6	15.4	952	14	BM917763
10	222.4	15.4	789	12	BG205056
11	211.6	14.7	884	12	BG182330
12	211.6	14.7	1167	14	BQ053936
13	207.4	14.4	876	13	BI906283
14	204.2	14.0	672	10	BB638766
15	202.4	14.0	745	12	BG204024
16	190.4	13.2	869	12	BF119225
17	187.4	13.0	568	12	BF193051
18	174	12.1	533	12	BF193021
19	170.2	11.8	669	13	BI939893
20	167.2	11.6	934	12	BG460984
21	166.4	11.5	639	10	BB629533
22	164.6	11.4	469	17	BB4215
23	162.4	11.3	863	13	BI661279
24	157.8	10.9	646	10	BB615654
25	157.8	10.9	662	10	BB644135
26	157.8	10.9	665	10	BB628567
27	157.8	10.9	723	14	BM951933
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29	157.8	10.9	936	12	BF119806
30	157.8	10.9	965	14	BQ944555
31	157.6	10.9	551	12	BF081124
32	156.2	10.8	600	13	BI987229
33	154.4	10.7	451	10	AW658666
34	149.6	10.4	3005	11	AK019478
35	146	10.1	669	10	BB642553
36	144.4	10.0	867	13	BI106339
37	139.4	9.7	650	10	BB630138
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39	138.4	9.6	450	14	W04836
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43	135	9.4	659	17	AZ667240
44	130	9.0	1098	17	CNS0586L
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ALIGNMENTS

RESULT 1
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LOCUS
DEFINITION
603045953f1 NIH_MGC_116 Homo sapiens cDNA clone IMAGE:5186388 5', mRNA sequence.
807 bp mRNA linear EST 25-SEP-2001
ACCESSION
BI764263
VERSION
BI764263.1
KEYWORDS
EST.
SOURCE
human.
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 (bases 1 to 807)
NIH-MGC <http://mgc.nci.nih.gov/>.
AUTHORS
National Institutes of Health, Mammalian Gene Collection (MGC)
TITLE
Unpublished (1999)
JOURNAL
COMMENT
Contact: Robert Strausberg, Ph.D.
Email: cgapsb@mail.nih.gov
Tissue Procurement: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>
Plate: LLAM11465 row: i column: 13
High quality sequence stop: 805.
Location/Qualifiers
1. .807

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/db_xref="taxon:9606"
/clone="IMAGE:5186388"
/clone_lib="NIH_MGC_116"
/lab_host="DH10B"
/notes="Organ: pooled colon, kidney, stomach; Vector:
PCMV-SPORE; Site_1: NotI; Site_2: EcoRV (destroyed); RNA
source anonymous pool of 3 colons, age 26 yo male, 49 yo
female, 71 yo male colon; 45 yo male kidney, and pool of 2
stomachs, 62 yo male and 70 yo female. Library is
oligo-dT primed and directionally cloned (EcoRV site is
destroyed upon cloning). Average insert size 1.4 kb,
insert size range 1-3 kb. Library is normalized and
enriched for full-length clones and was constructed by C.
Gruber (Invitrogen). Research Genetics tracking code
023. Note: this is a NIH_MGC Library."
BASE COUNT      186 a   209 c   171 g   241 t
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Query Match      45.4%; Score 654; DB 13; Length 807;
Best Local Similarity 94.8%; Pred. No. 7.5e-185;
Matches 743; Conservative 0; Mismatches 5; Indels 36; Gaps 5;
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DB 28 CCGCGGTGGAACAGATGATTATCAAGTGGAGTCCCAATCTATGACATCAATATTATTA 87
QY 284 TACATCGGAGCCCTGCCAAAATCAATGTGAAGCAATCGCAGCCGCTTCGTGCTCC 343
DB 88 TACATCGGAGCCCTGCCAAAATCAATGTGAAGCAATCGCAGCCGCTTCGTGCTCC 147
QY 344 GCTCTACTCAGTGGTTCATCTTTGTTTGTGGCAACATCTGTCATCTCCATCCCT 403
DB 148 GCTCTACTCAGTGGTTCATCTTTGTTTGTGGCAACATCTGTCATCTCCATCCCT 207
QY 404 GATAAATCGAAAGGCTGAAGACATGACTGACATCTACCTGCTCAACCTGGCCATCTC 463
DB 208 GATAAATCGAAAGGCTGAAGACATGACTGACATCTACCTGCTCAACCTGGCCATCTC 267
QY 464 TGACCTGTTTTCCTTCTACTGTCCCTTCCTGGGCTCAGTATGTCGGCCAGTGGGA 523
DB 268 TGACCTGTTTTCCTTCTACTGTCCCTTCCTGGGCTCAGTATGTCGGCCAGTGGGA 327
QY 524 CTTTGGAAATACAAATGTCTCAACTCTTGACAGGCTCTATTATTATAGGCTTCTCTCG 583
DB 328 C-TTGGAAATACAAATGTCTCAACTCTTGACAGGCTCTATTATTATAGGCTTCTCTCG 386
QY 584 AATCTTCTCATCATCTCTCTGCAATCGATAGTACCTGGCTGTGCTGCTCATGCTGTGT 643
DB 387 AATCTTCTCATCATCTCTCTGCAATCGATAGTACCTGGCTGTGCTGCTCATGCTGTGT 446
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DB 687 GGGAAATCCTTAAAGATCTGCTTGGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 745
QY 912 GCTTATCTTCCACATCATGATGTTTATTTTCTCTGCTGGGCTCCCTACAAATATGTCCT 971
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Db 746 GCTTATCTTCCACATCATGATGTTTATTTTCTCTGCTGGGCT-CCTACACATGTCCT 803
QY 972 TCTC 975
DB 804 TCTC 807
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RESULT 2
BE656336 487 bp mRNA linear EST 06-SEP-2000
LOCUS UI-M-BH0-aju-h-06-0-UI.r1 NIH_BMAP_M.S1 Mus musculus cDNA clone
DEFINITION UI-M-BH0-aju-h-06-0-UI 5', mRNA sequence.
ACCESSION BE656336
VERSION BE656336.1 GI:9982249
KEYWORDS EST.
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 487)
REFERENCE 1 (bases 1 to 487)
AUTHORS Ronaldo,M.F., Lennon,G. and Soares,M.B.
TITLE Normalization and subtraction: two approaches to facilitate gene
discovery
JOURNAL Genome Res. 6 (9), 791-806 (1996)
MEDLINE 9704477
COMMENT Contact: Chin, H
National Institute of Mental Health
6001 Executive Blvd. Room 7N-7190, MSC 9643, Bethesda, MD
20892-9643, USA
Tel: 301 443 1706
Fax: 301 443 9890
Email: mst@mail.nih.gov
cDNA Library Preparation: M.B. Soares Lab Clone distribution:
Researchers may obtain BMAP cDNA clones from RESEARCH GENETICS. It
should be noted that Bento Soares is generating a small number of
additional specialized non-redundant arrays of BMAP cDNAs whose
availability will be considered under appropriate and limited
collaborative arrangements
Seq primer: M13 Reverse.
Location/Qualifiers
1. 487
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/strain="C57BL/6J"
/db_xref="taxon:10090"
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/clone_lib="NIH_BMAP_M.S1"
/dev_stage="27-32 days"
/lab_host="DH10B (Life Technologies)"
/notes="Vector: pRT3D-Pac (Pharmacia) with a modified
polylinker; Site_1: Not I; Site_2: Eco RI; The
NIH_BMAP_M.S1 library is a subtracted library derived from
a mixture of normalized libraries from ten regions of the
mouse brain (cerebellum, brain stems, olfactory bulbs,
hypothalamus, cortex, amygdala, basal ganglia, pineal
gland, striatum, hippocampus). The driver used for
subtraction consisted of a pool of 20,000 cDNA clones
obtained from non-normalized and normalized libraries of
these ten regions of the mouse brain."
BASE COUNT      115 a   115 c   103 g   154 t
ORIGIN
Query Match      25.0%; Score 360.6; DB 10; Length 487;
Best Local Similarity 84.6%; Pred. No. 8.3e-97;
Matches 405; Conservative 0; Mismatches 74; Indels 0; Gaps 0;
QY 264 ATCTATGACATCAATATTATTATACATCGGAGCCCTGCCAAAATCAATGTGAAGCAATC 323
DB 9 AGCTATGACATCGATTATGATGTGTCAGCACCTGCCAAAATCAATGTGAAGCAAT 68
QY 324 GCAGCCCGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 383
DB 69 GCGGCTCAGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 128
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1248
 TGGGGCTCCCGAGCGAGCAAGCTCAGTTTACACCGGATCCACTGGGGAGCAGGAA

Qy


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||||| 181 GGCGTGGTGGCCAGCTGTGTCATGATGCTGTGTCATTCGGGATCATAAACCCCTG 240
|||||
QY 871 CTTTCGCTGTCGAATAGAGAGAGGACACAGGCTGTGAGGCTTATCTTCACCATCAG 930
|||||
Db 241 CTCGGTGTGCGACGAGAGAGAGACACAGGCTGTGAGGCTCATCTTCGTGATCAG 300
|||||
QY 931 ATTGTTTATTTCTTCCTTCCTGCTCCCTACACATTTGCTTCCTTCCTGACACCTTCCAG 990
|||||
Db 301 ATTGCTACTTTCCTTCCTTCCTGCTCCCTACACATTTGCTTCCTTCCTGACACCTTCCAG 360
|||||
QY 991 GAATCTTTGGCTTGAAT-AAATGCACTAGCTCTACAGGTTGGACCAAGCTATGAGGT 1049
|||||
Db 361 GAATCTTTGGCTTGAATAACTGCAGTGGCTCTACAGGCTGGACCAAGCTATGAGGT 420
|||||
QY 1050 GACAGAGACTTTGGGATGAGGACTGTGTCATCAACCCATCACTATGCTTTGTCGG 1109
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Db 421 GACAGAGACCTGGGGATGACGCACTGTGTCATCAACCCATCACTATGCTTTGTCGG 480
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RESULT 6
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LOCUS v104901.r2 Soares_mammary_gland_NBMWG Mus musculus cDNA clone
DEFINITION IMAGE:963216 5' similar to TR:G1322040 G1322040 C-C CHEMOKINE
RECEPTOR. ; mRNA sequence.
ACCESSION AA671573 GI:2643652
VERSION AA671573.1
SOURCE EST.
ORGANISM house mouse.
REFERENCE Mus musculus
AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 447)
Marras, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubuque, T.,
Geisel, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M.,
Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B.,
Theising, B., Wylie, T., Lennon, G., Soares, B., Wilson, R. and
Waterston, R.
The WashU-RHMI Mouse EST Project
Unpublished (1996)
Contact: Marra M/Mouse EST Project
WashU-RHMI Mouse EST Project
Washington University School
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL ; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
MGI:552008
Seq primer: -28ml3 rev2 ET from Amersham
High quality sequence stop: 397.
FEATURES
source
location/Qualifiers
1. .447
/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="IMAGE:963216"
/clone_lib="Soares_mammary_gland_NBMWG"
/sex="male"
/tissue_type="mammary gland"
/dev_stage="4 weeks"
/lab_host="DH108"
/note="Organ: mammary gland; Vector: pT73D-Pac (Pharmacia)
with a modified polylinker; Site_1: Not I; Site_2: Eco
RI; 1st strand cDNA was primed with a Not I - oligo(dT)
primer [5]
TGTTCACCAATCTGAGTGGGCGCGGGAATGGTGTGTTTTTTTTTTTTTTTTTTT
T 3']; double-stranded cDNA was ligated to Eco RI
adaptors (Pharmacia), digested with Not I and cloned into
the Not I and Eco RI sites of the modified pT73 vector.
RNA provided by Dr. Minoru Ko, Wayne State Univ. Library

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constructed and normalized by Bento Soares and M.Fatima
Bonaldo."
BASE COUNT 104 a 102 c 92 g 149 t
ORIGIN
Query Match 19.5%; Score 280.8; DB 9; Length 447;
Best Local Similarity 80.0%; Pred. No. 7.5e-73;
Matches 357; Conservative 0; Mismatches 57; Indels 32; Gaps 1;
QY 547 TCTTGACAGGGCTCTATTTTATAGGCTTCTCTCGGAATCTTCTTCATPCATCCTCCTGA 606
|||||
Db 2 TATTCACAGGGCTCTATCACAATGGTTATTTTGGTGGAACTCTTCATATCCTCTGA 61
|||||
QY 607 CAATCGATAGTAGTACCTGGCTCTGTCGATGCTGTGTTTGTCTTTAAAGCGAGGAGTCA 666
|||||
Db 62 CAATTTGATAGTACTTGGCTATTGCTCCATGCTGTGTTTGTCTTTAAAGTCAGAACGTCA 121
|||||
QY 667 CTTTGGGGTGTGCAAGTGTGATCAGTGGTGGTGGTGTGTTGGTCTCTCCAG 726
|||||
Db 122 ACTTTGGGGTGTATACAAGTAGTCACTTGGGCGGTGGTGTGTTGCCCTCTCCAG 181
|||||
QY 727 GAATCATCTTTTACAGATCTCTCAAAAGAGGTCCTTCATTCACCTCGAGCTCTCAT --- 782
|||||
Db 182 AAATAATCTTTACAGATCTCTCAGAAAGAGGTTTTCATTTACATCATGCTCTCATTTTC 241
|||||
QY 783 -----TTTCCATCATATTAAAGATGATCACTCTGGGC 814
|||||
Db 242 CACACACTCAGTATCATTTCTGGAAGAGTTTCCAAACATTTAAAGATGCTCATCTGAGCC 301
|||||
QY 815 TGGTCTCGCGCTGTGTCATGTCATCTGCTGCTGGAATCTTAAAGATCTGCTTC 874
|||||
Db 302 TGATCTCGCTCTACTTCTCATGTCATCTGCTACTCAGGAATCTCCACACCTGTTTC 361
|||||
QY 875 GGTGTCGAATGAGAAGAGGACAGGCTGTGAGGCTTATCTTCACCATCATGATTG 934
|||||
Db 362 GCTGTAGGAATGAGAAGAGGACAGGCTGTGAGGCTCATCTTTGCCATCATGATTG 421
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QY 935 TTATTTCTCTCTCTGGGCTCCCTAC 960
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Db 422 TCTACTTCTCTCTGGACTCCCTAC 447

RESULT 7
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LOCUS AL552677 LFL_NFL006_PL2 Homo sapiens cDNA clone CS0D1067YK08 5
DEFINITION prime, mRNA sequence.
ACCESSION AL552677
VERSION AL552677.1 GI:12891808
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 907)
Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
Full-length cDNA libraries and normalization
Unpublished (2001)
Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr.
FEATURES
source
location/Qualifiers
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/clone="CS0D1067YK08"
/clone_lib="LFL_NFL006_PL2"
/tissue_type="placenta"
/note="Vector: pCMVSPORT 6; Site_1: NotI; 1st strand cDNA
was primed with a NotI-oligo(dT) primer. Five prime end
enriched, double-stranded cDNA was digested with Not I and
cloned into the Not I and Eco RV sites of the pCMVSPORT 6

```


Tel: 216 431 9900			
Fax: 216 361 9596			
Email: scai@ethersys.com			
High quality sequence stop: 521.			
Location/Qualifiers			
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/notes="See 'Creation of Genome-Wide Protein Expression Libraries using Random Activation of Gene Expression', Nature Biotechnology, in press. Note that even though the cell type indicated is H1080, since a random activation method was used, these sequence tags are not necessarily expressed in H1080 under normal circumstances."			
BASE COUNT	174 a	202 c	222 t
ORIGIN			
Query Match	15.4%;	Score 222.4;	DB 12; Length 789;
Best Local Similarity	61.5%;	Pred. No. 3.4e-55;	
Matches 426;	Conservative	0;	Mismatches 229; Indels 38; Gaps 3;
QY	293	GCCTGCCAATAAATCAATGTAAGCAATPCGACGGCGCTCTCGCTCGCTCGCTCACTAC	352
Db	81	GCTCTGTGAAAAGCTGATACAGACCACTGATGGCCAGTTTGTGCCCCCGCTGACTC	140
QY	353	ACTGTGTTTCATCTTTGTTTGGGCAACATGTGTCATCTTCATCCTCACTCGATTAAC	412
Db	141	CTGTGTTTCACTGTGGGCGCTCTTGGGCAATGTGTTGGTGATGATCTTCATTAATA	200
QY	413	CAAAAGGTGAAGAGCATGACTGATCTACCTGCTCAACCTGGCGCATCTCTGACCTGT	472
Db	201	CAGGAGCGTCGGAATTAATGACCAACATCACTGCTCAACTGGCCATTTGGACCTGT	260
QY	473	TTTCTCTTACTGTCCTCTGCGGCTCACTATGCTGCTGGCGCC--ASTGGGNCITTTG	529
Db	261	CTTCTCTGTCACCTTCCATCTCGATCGACATGCTGAGGGGCACTACTGGGTTT	320
QY	530	AAATAAATGTCGAACCTTTGACAGGCTCTATTTATAGGCTTCTTCTCTGGAATCT	589
Db	321	CCATGGCATGCTGAAGTCTCTCTCAGSGTTTATCACACAGGCTGTACACGAGATCT	380
QY	590	CTTCATCATCTCTCTGCACAACTGATAGTACTGCTGCTGCTGCTGCTGCTGCTGCT	649
Db	381	TTTCATAATCTGCTCACAATCGACAGGACCTGGCCATTGCCATGCTGTGATTCGCT	440
QY	650	AAAGCCAGGACGGTCACTTTGGGGTGGTGACAAGTGTGATCACTTGGGTGGTGGCTG	709
Db	441	TCGAGCCGGAGTCTCACTTTTGGTGTCACTACCAGCATCGTCACTGGGCGCTGGCA	500
QY	710	GTTTGGGTCTCTCCAGGAATCATCTTACCAGATCTCAAAAGAGAGTCTTCATTAAC	769
Db	501	GCTAGCAGCTCTCTCTGGAATTAATCTCTATGAGACCGAAGTGTGTTGAGAGACT	560
QY	770	CTGCAGCTCTCAT-----TTTCCATACATATAA	797
Db	561	NTGCAGTCTCTTTACCCAGAGGATACAGTATATAGCTGGAGGCATTTCCACACTG	620
QY	798	GATAGTCACTTTGGGCTGGTCTGCGCGTGTCTGTCATGGTCACTGCTACTCGGGA	857
Db	621	AATGACCGCTCTCTGCTCTGCTCTCCCTGCTGCTGCTGCTGATGAGCCATCTG	680
QY	858	CTTAATAACTCTGTTCCGGTGTGCAAAATGAGAGAGGACAGGGCTGTGAGGCTTAT	917
Db	681	CATCANACGCTGCTGAGTGCGCCAGT---AAAAAAGTCAAGGCCATCCGGCTCAT	737
QY	918	CTTCAACATCAATGTTTATTTCTTCTCTG	950
Db	738	TTNTGTCATCATGGGGGGTCTTTTCATTTCTG	770

RESULT 11

BG182330	BG182330	884 bp	mRNA	linear	EST 21-APR-2001
LOCUS	RST1196	Athersys RAGE Library Homo sapiens cDNA, mRNA sequence.			
DEFINITION	BG182330				
ACCESSION	BG182330.1	GI:13704017			
VERSION	EST.				
KEYWORDS	human.				
SOURCE	Homo sapiens				
ORGANISM	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.				
REFERENCE	1 (bases 1 to 884)				
AUTHORS	Harrington,J.J., Sherf,B., Rundlett,S., Jackson,P.D., Perry,R., Cain,S., Leventhal,C., Thornton,M., Ramachandran,R., Whittington,J., Lerner,L., Costanzo,D., McElligott,K., Boozer,S., Mays,R., Smith,E., Veloso,N., Klifa,A., Hess,J.G., Cothren,K., Lo,K.K., Offenbacher,J., Danzig,J. and Ducar,M.				
TITLE	Creation of genome-wide protein expression libraries using random activation of gene expression				
JOURNAL	Nat. Biotechnol. 19 (5), 440-445 (2001)				
MEDLINE	21227151				
COMMENT	Contact: Scott J. Cain Athersys, Inc. 3201 Carnegie Ave, Cleveland, OH 44115, USA Tel: 216 431 9900 Fax: 216 361 9596 Email: scain@atersys.com High quality sequence stop: 529. Location/Qualifiers 1..884 /organism="Homo sapiens" /db_xref="taxon:9606" /clone_lib="Athersys RAGE Library" /cell_line="Hr1080" /note="See 'Creation of Genome-wide Protein Expression Libraries Using Random Activation of Gene Expression', Nature Biotechnology, in press. Note that even though the cell type indicated is Hr1080, since a random activation method was used, these sequence tags are not necessarily expressed in Hr1080 under normal circumstances."				
FEATURES	source				
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	Best local Similarity	60.9%;	Pred. No. 6.4e-52;		
	Matches 436;	Conservative	0;	Mismatches 239;	Indels 41; Gaps 4;
QY	293	GCCCTGCCAAATAATCAATGTGAAGCAAATPCGACCGCGCTCCTGCCTGGCTACTAC TC 352			
Db	82	GCCTGTGAAAAGCTGATPACCAGAGCACTGATGCCCACTTTTGTGCCCGCGCTGACTC 141			
QY	353	ACTGGTGTTTCATCTTTGGTTTGTGGCAACAATGCTGGTCATCCTCATCTCTGATAAAC TG 412			
Db	142	CCTGGTGTTCACCTGTGGGCGCTTTTGGCAATGTGGTGGTGATGATCTCTCATATAAATA 201			
QY	413	CAAAAGGCTGAAGAGCATGACTGATCATCTACTCTGCTCAACCTGGCCACTCTGCACCTGT T 472			
Db	202	CAGGAGGCTCCGAATTATGACACATCTACCTGCTCACTGGCCATTTCCGACTGCTG 261			
QY	473	TTTTCTCTTTACTGTCCCCCTTCTGGGCTCACTACTGCTGCCGCC --- AGTGGGACTTTGG 529			
Db	262	CTTCTCTGTCACCTCTCCATTTCTGSATCCACTATGTCAGGGGGGCATAC TACTGGTTTTGG 321			
QY	530	AAATACATGTGTCACTCTTGACAGGGCTCTATTTTATAGGCTTCTTCTCTGGAATCT 589			
Db	322	CCATGGCATGTGTAAGCTCCTCTCAAGGTTTTATCACACAGGCTTGTACAGCGAGATCT 381			
QY	590	CTTTCATCATCTCTCTGACAAATCGATAGGTACTGCTGCTCGTCAATGCTGTGTTTCTTT 649			
Db	382	TTTCATATCTCTGTGACAAATGCAGGTACTGCGCCATTTGTCCATGCTGTGTTCGCT 441			
QY	650	AAAAGCCAGAGCGGTCACTCTTTGGGGTGGTGACAAAGTGTATCATTGGGTGGTGGCTGT 709			
Db	442	TCGACCCGGGACTGTCACTTTTGGTGTGTCATCACACAGATCGTCACTGGGGCGCTGCACT 501			

non-activated adult donors. Library is oligo-dT primed and directionally cloned (forky site is destroyed upon cloning). Average insert size 1.7 Kb, insert size range 1.2-3.3 kb. Library is normalized and enriched for full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 027. Note: this is a NIH_MGC Library."

BASE COUNT 202 a 232 c 193 g 249 t
ORIGIN

Query Match 14.4%; Score 207.4; DB 13; Length 876;

Best Local Similarity 61.2%; Pred. No. 1.2e-50;

Matches 441; Conservative 0; Mismatches 241; Indels 39; Gaps 5;

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QY 293 GCCCTGCCAAAATCAATGTCAGCAAAATGCGACCGCGCTCTCTCCCTCGCTCTACTC 352
DB 144 GCTCTGTGAAAGAGCTGATACACAGACATGATGCCGACGTTGTGCCCGCGCTACTC 203
QY 353 ACTGGTGTTCATCTTTGGTGGGCAACATGCTGTCTATCTCTCATCTCTGATATAACTG 412
DB 204 CTTGGTGTCTACTGTGGGCTCTTGGGCAATGCTGTGTGTGTATCTCTCATATAATA 263
QY 413 CAAAGGCTGAAGAGCATGACTACATCACTACCTGTCTCACTGCGCATCTGTGACCTGT 472
DB 264 CAGGAGGCTCCGAATATGACCAACATCTACCTGTCTCACTGCGCATCTGTGACCTGT 323
QY 473 TTTCTCTTCTTACTGTCCTCTTGGGCTCACTATCTCTGCGGCTCTCTCTCTCTCT 529
DB 324 CTTCTCTCTTCTTACTGTCCTCTTGGGCTCACTATCTCTGCGGCTCTCTCTCTCTCT 383
QY 530 AAATACATATGTCACATCTTTCAGGCGCTCTATTTATAGGCTCTCTCTCTCTCTCT 589
DB 384 CCATGGCATCTGTAGCTCTCTCTCAGGCTTTTATCACAGGCTTGTACAGGAGACTT 443
QY 590 CTTATCATCTCTCTGACATCACTAGTACCTGCTCTCTCTCTCTCTCTCTCTCTCT 649
DB 444 TTTCTATCTCTCTGACATCACTAGTACCTGCTCTCTCTCTCTCTCTCTCTCTCT 503
QY 650 AAAAGCCAGGAGCTGCTCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 709
DB 504 TCGAGCCGCGACTGTCTACTTATGCTGTCTACACAGCATCTGCTCACTGGGCGCTGG 563
QY 710 GTTGGCTCTCTCCAGGATCACTCTTACAGATCTCTCAAAAGAGGCTCTTCAATAC 769
DB 564 CTTAGCAGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 623
QY 770 CTGACGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 797
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QY 798 GATAGTCATCTGGGCTGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 856
DB 684 AATGACCATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 743
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DB 744 TCTTAAAGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 801
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QY 977 T 977
DB 861 T 861
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RESULT 14

BB638766

LOCUS

BB638766 RIKEN full-length enriched, 3 days neonate thymus Mus

musculus cdna clone A630052D16 5', mRNA sequence.

ACCESSION

BB638766

VERSION
KEYWORDS
SOURCE
ORGANISMREFERENCE
AUTHORSTITLE
JOURNAL
COMMENTFEATURES
source

BB638766.1 GI:16474321
EST.
house mouse.
Mus musculus
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 672)
Arakawa,T., Carninci,P., Fukuda,S., Furuno,M., Hanagaki,T., Hara,A.,
Hiramoto,K., Hori,F., Ishii,Y., Ito,M., Kawai,J., Konno,H., Kouda,
M., Koya,S., Matsuyama,T., Miyazaki,A., Nomura,K., Ohno,M.,
Okazaki,Y., Okido,T., Saito,T., Sakai,C., Sakai,K., Sano,H., Sasaki,
D., Shibata,K., Shinagawa,A., Shiraki,T., Sogabe,Y., Suzuki,H.,
Tagami,M., Tagawa,A., Takahashi,F., Takeda,Y., Tanaka,T., Toyota,T.,
Muramatsu,M. and Hayashizaki,Y.
RIKEN Mouse ESTs (Arakawa,T., et al. 2001)
Unpublished (2001)
Contact: Yoshihide Hayashizaki
Laboratory for Genome Exploration Research Group, RIKEN Genomic
Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
Tel: 81-45-503-9222
Fax: 81-45-503-9216
Email: genome-res@gsr.riken.go.jp,
URL:http://genome.gsc.riken.go.jp/
Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh,
M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new
genes. Genome Res. 10 (10), 1617-1630 (2000)
wagi,K., Fujiwaki,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E.,
Watabiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsura,
S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and
Hayashizaki,Y.
RIKEN integrated sequence analysis (RISA) system-384-format
sequencing pipeline with 384 multicapillary sequencer. Genome Res.
10 (11), 1757-1771 (2000)
Konno,H., Fukunishi,Y., Shibata,K., Itoh,M., Carninci,P., Sugahara,
Y. and Hayashizaki,Y.
Computer-based methods for the mouse full-length cDNA
encyclopedia: real-time sequence clustering for construction of a
nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)
Kondo,S., Shinagawa,A., Saito,T., Kiyosawa,H., Yamanaka,I., Alzawa,
K., Fukuda,S., Hara,A., Itoh,M., Kawai,J., Shibata,K. and
Hayashizaki,Y.
Computational Analysis of Full-length Mouse cDNAs Compared with
Human Genome Sequences. Mamm. Genome. 12, 673-677 (2001)
Please visit our web site (http://genome.gsc.riken.go.jp) for
further details.
e mouse tissues.
Location/Qualifiers
1. .672
/organism="Mus musculus"
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/dev_stage="3 days neonate"
/lab_host="DH10B"
/note="Site_1: SalI; Site_2: BamHI; cDNA library was
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Project of Genome Exploration Research Group in Riken
Genomic Sciences Center and Genome Science Laboratory in
RIKEN, Division of Experimental Animal Research in Riken
contributed to prepare mouse tissues. 1st strand cDNA was
primed with a primer [5'
GAGAGAGAGAGATCCAGAGCTCTTTTTTTTTTTTTTTTNN 3'], cDNA was
prepared by using trehalose thermo-activated reverse
transcriptase and subsequently enriched for full-length by
cap-trapper. cDNA went through one round of normalization
to Rot = 20.0 and subtraction to Rot = 459.0. Second
strand cDNA was prepared with the primer adapter of

